```
                GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on:     April  3, 2005, 20:59:14 ; Search time 2144.82 Seconds
                                         (without alignments)
                            6031.995 Million cell updates/sec

Title:      US-10-088-666-1
Perfect score: 267
Sequence:   267  1 tatatggaagtaagacccct.........agtagttggggggatcgcccc 267
Scoring table: IDENTITY_NUC
            Gapop 10.0 , Gapext 1.0

Searched:   4708233 seqs, 2422607955 residues
Total number of hits satisfying chosen parameters:        9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     GenEmbl:*
          1:  gb_ba:*
          2:  gb_htg:*
          3:  gb_in:*
          4:  gb_om:*
          5:  gb_ov:*
          6:  gb_pat:*
          7:  gb_ph:*
          8:  gb_pl:*
          9:  gb_pr:*
         10:  gb_ro:*
         11:  gb_sts:*
         12:  gb_sy:*
         13:  gb_un:*
         14:  gb_vi:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	267	100.0	267	6	AX105729	AX105729 Sequence
2	173.4	64.9	269050	1	AL935255	AL935255 Lactobaci
c 3	173.4	64.9	297050	1	AL935258	AL935258 Lactobaci
c 4	171.8	64.3	298050	1	AL935260	AL935260 Lactobaci
c 5	171.8	64.3	298050	1	AL935261	AL935261 Lactobaci
6	171.8	64.3	324050	1	AL935253	AL935253 Lactobaci
7	156.4	58.6	317	6	AX105734	AX105734 Sequence
8	156.4	58.6	317	6	AX105735	AX105735 Sequence
9	143.6	53.8	326	6	AX105730	AX105730 Sequence
10	139.4	52.2	335	6	AX105737	AX105737 Sequence
11	138.2	51.8	326	6	AX105738	AX105738 Sequence
12	136.4	51.1	336	6	AX105736	AX105736 Sequence
c 13	131	49.1	177911	1	AE017206	AE017206 Lactobaci
c 14	131	49.1	183043	6	AX926717	AX926717 Sequence
15	131	49.1	300478	1	AE017201	AE017201 Lactobaci
c 16	131	49.1	300886	1	AE017205	AE017205 Lactobaci
17	131	49.1	349980	6	AX926712	AX926712 Sequence
18	131	49.1	349980	6	AX926713	AX926713 Sequence
19	119.2	44.6	338	6	AX105733	AX105733 Sequence
c 20	115.8	43.4	31702	6	AX413012	AX413012 Sequence
c 21	115.6	43.3	3510	6	CQ788962	CQ788962 Sequence
c 22	115.6	43.3	3510	6	AR218821	AR218821 Sequence
c 23	115.6	43.3	3510	6	BD003733	BD003733 Polynucle
c 24	115.6	43.3	3989	6	BD193765	BD193765 Enterococ
25	115.6	43.3	5048	6	BD263589	BD263589 Novel str
26	115.6	43.3	8411	6	AX343071	AX343071 Sequence
27	115.6	43.3	8411	6	CQ788925	CQ788925 Sequence
28	115.6	43.3	8411	6	AR218784	AR218784 Sequence
29	115.6	43.3	8411	6	BD003696	BD003696 Polynucle
c 30	115.6	43.3	9873	1	AE007481	AE007481 Streptoco
c 31	115.6	43.3	10058	1	AE007489	AE007489 Streptoco
32	115.6	43.3	10551	1	AE007319	AE007319 Streptoco
c 33	115.6	43.3	10557	1	AE008537	AE008537 Streptoco
c 34	115.6	43.3	10856	1	AE008546	AE008546 Streptoco
c 35	115.6	43.3	11385	1	AE007495	AE007495 Streptoco
36	115.6	43.3	11660	6	AE008386	AE008386 Streptoco
37	115.6	43.3	11915	6	CQ789005	CQ789005 Sequence
38	115.6	43.3	11915	6	AR218864	AR218864 Sequence
39	115.6	43.3	11915	6	BD003776	BD003776 Polynucle
40	115.6	43.3	137952	2	SPNEU1909	AL449931 Streptoco
41	115.6	43.3	232807	2	SPNEU1901	AL449923 Streptoco
42	115.6	43.3	301488	1	AE016950	AE016950 Enterococ
c 43	115.6	43.3	304454	1	AE016956	AE016956 Enterococ
c 44	115.6	43.3	349980	6	AX571765	AX571765 Sequence
c 45	115.6	43.3	349980	6	AX571766	AX571766 Sequence

ALIGNMENTS

```
RESULT 1
AX105729
LOCUS       AX105729                267 bp    DNA    linear   PAT 30-APR-2001
DEFINITION  Sequence 1 from Patent WO0123605.
ACCESSION   AX105729
VERSION     AX105729.1  GI:13921742
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                    GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:      April  3, 2005, 20:53:24 ; Search time 926.081 Seconds
                                         (without alignments)
                                         1706.731 Million cell updates/sec

Title:           US-10-088-666-1
Perfect score:   267
Sequence:        1 tatatggaagtaagaccct........agtagttggggatcgcccc 267

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        439206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters:     8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       N_Geneseq_16Dec04:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
                 3: geneseqn2000s:*
                 4: geneseqn2001as:*
                 5: geneseqn2001bs:*
                 6: geneseqn2002as:*
                 7: geneseqn2002bs:*
                 8: geneseqn2003as:*
                 9: geneseqn2003bs:*
                10: geneseqn2003cs:*
                11: geneseqn2003ds:*
                12: geneseqn2004as:*
                13: geneseqn2004bs:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	267	100.0	267	5	AAF61566	Aaf61566 Lactobaci
2	156.4	58.6	317	5	AAF61572	Aaf61572 L. coryni
3	156.4	58.6	317	5	AAF61571	Aaf61571 L. coryni
4	143.6	53.8	326	5	AAF61567	Aaf61567 Lactobaci
5	139.4	52.2	335	5	AAF61574	Aaf61574 Pediococc
6	138.2	51.8	326	5	AAF61575	Aaf61575 Pediococc
7	136.4	51.1	336	5	AAF61573	Aaf61573 Lactobaci
8	131	49.1	110000	10	ADF77343_05	Continuation (6 of
9	131	49.1	110000	10	ADF77343_07	Continuation (8 of
c 10	131	49.1	110000	10	ADF77343_18	Continuation (19 o
11	121.6	45.5	110000	9	ADB12064_00	Adb12064 Alloiococ
c 12	120	44.9	110000	9	ADB12064_05	Continuation (6 of
c 13	120	44.9	110000	9	ADB12064_14	Continuation (15 o
14	119.2	44.6	338	5	AAF61570	Aaf61570 Lactobaci
15	116.8	43.7	110000	6	ADB12064_04	Continuation (5 of
c 16	115.8	43.4	31702	6	ABQ67190	Abq67190 Listeria
c 17	115.6	43.3	3510	2	AAV52186	Aav52186 Streptoco
c 18	115.6	43.3	3989	6	AAX13296	Aax13296 Enterococ
c 19	115.6	43.3	3989	6	ABS99091	Abs99091 Enterococ
c 20	115.6	43.3	5048	3	AAA65735	Aaa65735 Streptoco
21	115.6	43.3	5048	6	ABK15101	Abk15101 DNA encod
22	115.6	43.3	8411	2	AAV52149	Aav52149 Streptoco
23	115.6	43.3	11915	2	AAV52229	Aav52229 Streptoco
c 24	115.6	43.3	110000	10	ABS56454_16	Continuation (17 o
c 25	115.6	43.3	110000	10	ABS56454_17	Continuation (18 o
c 26	115.6	43.3	110000	10	ABS56454_18	Continuation (19 o
27	115.6	43.3	110000	10	ABS56454_20	Continuation (21 o
c 28	114.2	42.8	1389	6	ABQ70505	Abq70505 Listeria
c 29	114.2	42.8	2631	6	ABQ67189	Abq67189 Listeria
30	114.2	42.8	5349	6	ABQ70982	Abq70982 Listeria
c 31	114.2	42.8	110000	6	ABQ67196_0	Abq67196 Listeria
32	114.2	42.8	110000	6	ABQ67196_5	Continuation (6 of
33	114.2	42.8	110000	6	ABQ69245_02	Continuation (3 of
c 34	114.2	42.8	110000	6	ABQ69245_17	Continuation (18 o
c 35	114.2	42.8	110000	6	ABQ69245_18	Continuation (19 o
c 36	114.2	42.8	110000	6	ABQ69245_19	Continuation (20 o
c 37	114.2	42.8	110000	6	ABQ69245_24	Continuation (25 o
c 38	114.2	42.8	110000	6	ABQ69245_27	Continuation (28 o
c 39	114.2	42.8	110000	6	ABQ67197_01	Continuation (2 of
40	114.2	42.8	110000	6	ABA03041_02	Continuation (3 of
c 41	114.2	42.8	110000	6	ABA03041_24	Continuation (25 o
c 42	114.2	42.8	110000	6	ABA03041_26	Continuation (27 o
43	114.2	42.8	319630	6	ABQ67194	Abq67194 Listeria
c 44	114	42.7	9797	2	AAX13487	Aax13487 Enterococ
c 45	114	42.7	9797	6	ABS99282	Abs99282 Enterococ

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OM nucleic - nucleic search, using sw model

Run on: April 3, 2005, 22:12:40 ; Search time 271.009 seconds
                                     (without alignments)
                                     1612.071 Million cell updates/sec

Title: US-10-088-666-1
Perfect score: 267
Sequence: 1 tatatggaagtaagaccct.........agtagttgggggatcgcccc 267

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued Patents NA:*
                 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
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                 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                 5: /cgn2_6/ptodata/1/ina/pCTUS_COMB.seq:*
                 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	115.6	43.3	3510	3	US-08-961-527-53	Sequence 53, Appl
c	2	115.6	43.3	8411	3	US-08-961-527-16	Sequence 16, Appl
c	3	115.6	43.3	11915	3	US-08-961-527-96	Sequence 96, Appl
c	4	111.8	41.9	2725	4	US-09-710-279-3512	Sequence 3512, Ap
c	5	111.8	41.9	2869	4	US-09-710-279-4402	Sequence 4402, Ap
c	6	111.8	41.9	3012	4	US-09-710-279-3707	Sequence 3707, Ap
	7	111.8	41.9	3019	4	US-09-710-279-3918	Sequence 3918, Ap
	8	111.8	41.9	3232	4	US-09-710-279-4217	Sequence 4217, Ap
	9	111.8	41.9	3305	4	US-09-710-279-4156	Sequence 4156, Ap
c	10	111.8	41.9	3332	4	US-09-710-279-4283	Sequence 4283, Ap
c	11	111.8	41.9	3405	4	US-09-710-279-3903	Sequence 3903, Ap
c	12	111.8	41.9	3608	4	US-09-710-279-3759	Sequence 3759, Ap
c	13	111.8	41.9	3625	4	US-09-710-279-3658	Sequence 3658, Ap
c	14	111.8	41.9	3656	4	US-09-710-279-3739	Sequence 3739, Ap
c	15	111.8	41.9	3845	4	US-09-710-279-3520	Sequence 3520, Ap
c	16	111.8	41.9	4106	4	US-09-710-279-3684	Sequence 3684, Ap
c	17	111.6	41.8	840	4	US-08-956-171E-508	Sequence 508, Appl
c	18	111.6	41.8	840	4	US-08-781-986A-508	Sequence 508, Appl
c	19	110.2	41.3	1089	4	US-09-710-279-4333	Sequence 4333, Ap
c	20	110.2	41.3	3012	4	US-09-710-279-3683	Sequence 3683, Ap
c	21	110.2	41.3	3030	4	US-09-710-279-3916	Sequence 3916, Ap
c	22	110.2	41.3	3937	4	US-09-710-279-3772	Sequence 3772, Ap
c	23	109.6	41.0	400	4	US-08-956-171E-3738	Sequence 3738, Ap
c	24	109.6	41.0	400	4	US-08-781-986A-3738	Sequence 3738, Ap
c	25	108.6	40.7	2662	4	US-09-710-279-4334	Sequence 4334, Ap
c	26	106	39.7	400	4	US-08-956-171E-3624	Sequence 3624, Ap
c	27	106	39.7	400	4	US-08-781-986A-3624	Sequence 3624, Ap
c	28	105.6	39.6	1781	4	US-09-902-540-180	Sequence 180, App
c	29	104.4	39.1	386	4	US-08-956-171E-4064	Sequence 4064, Ap
c	30	104.4	39.1	386	4	US-08-781-986A-4064	Sequence 4064, Ap
c	31	101.2	37.9	6591	4	US-08-956-171E-3114	Sequence 3114, Ap
c	32	101.0	37.9	6591	4	US-08-781-986A-3114	Sequence 3114, Ap
c	33	100.8	37.8	400	4	US-08-781-986A-3768	Sequence 3768, Ap
c	34	100.6	37.7	400	4	US-08-781-986A-3768	Sequence 3768, Ap
c	35	100.6	37.7	400	4	US-08-956-171E-3638	Sequence 3638, Ap
c	36	100.6	37.7	400	4	US-08-956-171E-3748	Sequence 3748, Ap
c	37	100.6	37.7	400	4	US-08-781-986A-3638	Sequence 3638, Ap
c	38	100.6	37.7	400	4	US-08-781-986A-3748	Sequence 3748, Ap
c	39	100.6	37.7	458	4	US-08-956-171E-3757	Sequence 3757, Ap
c	40	100.6	37.7	458	4	US-08-781-986A-3757	Sequence 3757, Ap
c	41	100.6	37.7	15249	4	US-08-956-171E-102	Sequence 102, App
c	42	100.6	37.7	15249	4	US-08-781-986A-102	Sequence 102, App
	43	100.6	37.7	30246	4	US-08-956-171E-56	Sequence 56, Appl
	44	100.6	37.7	30246	4	US-08-781-986A-56	Sequence 56, Appl
c	45	100.4	37.6	400	4	US-08-956-171E-3611	Sequence 3611, Ap

ALIGNMENTS

RESULT 1
US-08-961-527-53/c
; Sequence 53, Application US/08961527

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OM nucleic - nucleic search, using sw model

Run on: April 3, 2005, 23:20:50 ; Search time 5972.62 Seconds
(without alignments)
270.571 Million cell updates/sec

Title: US-10-088-666-1
Perfect score: 267
Sequence: 1 tatatggaagtaagacccct........agtagttggggatcgcccc 267

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5607317 seqs, 302624599 residues

Total number of hits satisfying chosen parameters: 11214634

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

ALIGNMENTS

SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.		Score	Query % Match	Length	DB	ID	Description
c	1	115.8	43.4	31702	17	US-10-398-221-3	Sequence 3, Appli
c	2	115.6	43.3	3510	8	US-08-961-527-53	Sequence 53, Appl
c	3	115.6	43.3	3510	17	US-10-158-844-53	Sequence 53, Appl
c	4	115.6	43.3	3989	9	US-09-070-927A-359	Sequence 359, Appl
	5	115.6	43.3	5048	10	US-09-884-465A-2	Sequence 2, Appli
	6	115.6	43.3	8411	8	US-08-961-527-16	Sequence 16, Appl
	7	115.6	43.3	8411	17	US-10-158-844-16	Sequence 16, Appl
	8	115.6	43.3	11915	8	US-08-961-527-96	Sequence 96, Appl
	9	115.6	43.3	11915	17	US-10-158-844-96	Sequence 96, Appl
	10	115.6	43.3	2162598	19	US-10-472-928-4979	Sequence 4979, Appl
c	11	115.6	43.3	2162598	19	US-10-472-928-4979	Sequence 4979, Ap
c	12	114.2	42.8	1389	17	US-10-398-221-3318	Sequence 3318, Ap
c	13	114.2	42.8	2631	17	US-10-398-221-2	Sequence 2, Appli
	14	114.2	42.8	5349	17	US-10-398-221-3795	Sequence 3795, Ap
	15	114.2	42.8	319630	17	US-10-398-221-7	Sequence 7, Appli
	16	114.2	42.8	684707	17	US-10-398-221-9	Sequence 9, Appli
c	17	114.2	42.8	684707	17	US-10-398-221-9	Sequence 9, Appli
	18	114.2	42.8	1163020	17	US-10-398-221-10	Sequence 10, Appl
	19	114.2	42.8	3011208	17	US-10-398-221-2058	Sequence 2058, Ap
c	20	114.2	42.8	3011208	17	US-10-398-221-2058	Sequence 2058, Ap
c	21	114	42.7	9797	9	US-09-070-927A-550	Sequence 550, App
	22	114	42.7	22960	9	US-09-070-927A-345	Sequence 345, App
c	23	113.2	42.4	882	17	US-10-398-221-3395	Sequence 3395, Ap
c	24	113.2	42.4	1907	17	US-10-398-221-1847	Sequence 1847, Ap
	25	113.2	42.4	4199	17	US-10-398-221-3890	Sequence 3890, Ap
	26	113.2	42.4	6625	17	US-10-398-221-2041	Sequence 2041, Ap
	27	111.6	41.8	840	8	US-08-781-986A-508	Sequence 508, App
	28	111.6	41.8	840	8	US-10-329-624-508	Sequence 508, App
c	29	109.6	41.0	400	8	US-08-781-986A-3738	Sequence 3738, Ap
c	30	109.6	41.0	400	17	US-10-329-624-3738	Sequence 3738, Ap
c	31	106	39.7	400	8	US-08-781-986A-3624	Sequence 3624, Ap
c	32	106	39.7	400	17	US-10-329-624-3624	Sequence 3624, Ap
c	33	104.4	39.1	386	8	US-08-781-986A-4064	Sequence 4064, Ap
c	34	104.4	39.1	386	17	US-10-329-624-4064	Sequence 4064, Ap
c	35	101.2	37.9	6591	8	US-08-781-986A-3114	Sequence 3114, Ap
c	36	101.2	37.9	6591	17	US-10-329-624-3114	Sequence 3114, Ap
c	37	100.8	37.8	400	8	US-08-781-986A-3768	Sequence 3768, Ap
c	38	100.8	37.8	400	17	US-10-329-624-3768	Sequence 3768, Ap
c	39	100.6	37.7	400	8	US-08-781-986A-3638	Sequence 3638, Ap
c	40	100.6	37.7	400	8	US-08-781-986A-3748	Sequence 3748, Ap
c	41	100.6	37.7	400	17	US-10-329-624-3638	Sequence 3638, Ap
c	42	100.6	37.7	400	17	US-10-329-624-3748	Sequence 3748, Ap
c	43	100.6	37.7	458	8	US-08-781-986A-3757	Sequence 3757, Ap
c	44	100.6	37.7	458	17	US-10-329-624-3757	Sequence 3757, Ap
c	45	100.6	37.7	5134	19	US-10-857-625-162	Sequence 162, App

```
                    GenCore version 5.1.6
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-OM nucleic - nucleic search, using sw model

Run on:      April 3, 2005, 22:11:20 ; Search time 7983.54 Seconds
                                       (without alignments)
                            1273.014 Million cell updates/sec

Title:       US-10-088-666-1
Perfect score: 267
Sequence:    1 tatatggaagtaagacccct.........agtagttggggatcgcccc 267

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched:    3239544 seqs, 1903213700 residues

Total number of hits satisfying chosen parameters:   68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    EST:*
              1:  gb_est1:*
              2:  gb_est2:*
              3:  gb_htc:*
              4:  gb_est3:*
              5:  gb_est4:*
              6:  gb_est5:*
              7:  gb_est6:*
              8:  gb_gss1:*
              9:  gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

	Result No.	Score	% Match	Query Length	DB	ID	Description
	1	163.4	61.2	793	8	BZ369094	BZ369094 Cot100.1.
	2	105.4	39.5	3268	8	BH770998	BH770998 LLMGtag72
	3	105.4	39.5	6499	8	BH771024	BH771024 LLMGtag74
c	4	58.2	21.8	342	7	CR469421	CR469421 CR469421
	5	56.4	21.1	690	8	BH687637	BH687637 BOMA057TR
c	6	51.6	19.3	277	7	CR477397	CR477397 CR477397
	7	50.4	18.9	1258	8	BH770957	BH770957 LLMGtag68
	8	50.2	18.8	391	8	AQ990586	AQ990586 Rfc01382
c	9	50.2	18.8	607	8	AQ989492	AQ989492 Rfc00040
	10	49.2	18.4	393	8	CC144308	CC144308 B3 Neisse
c	11	49.2	18.4	453	5	BU003208	BU003208 QG34H04.
c	12	48.6	18.2	833	9	CL659016	CL659016 PRI0132d
	13	48.6	18.2	844	9	CL664279	CL664279 PRI0146c
c	14	48.6	18.2	872	9	CL662374	CL662374 PRI0141b
	15	48.6	18.2	879	9	CL667131	CL667131 PRI0154b
c	16	47.2	17.7	255	8	BH770635	BH770635 LLMGtag39
c	17	47.2	17.7	333	7	CR470260	CR470260 CR470260
	18	47	17.6	698	9	AG613316	AG613316 Escherich
	19	46	17.2	534	9	CL681720	CL681720 PRI0131d
c	20	46	17.2	664	9	AG613279	AG613279 Escherich
c	21	46	17.2	735	9	CL667389	CL667389 PRI0155a
	22	45.8	17.2	544	8	AQ989631	AQ989631 Rfc00197
	23	45.8	17.2	655	8	AQ990982	AQ990982 Rfc01832
c	24	44.8	16.8	1073	8	AF114216	AF114216 AF114216
c	25	44.4	16.6	646	9	CL660916	CL660916 PRI0138b
c	26	44.4	16.6	685	9	CL656043	CL656043 PRI0125c
c	27	44.4	16.6	786	9	CL654528	CL654528 PRI0120d
c	28	44.4	16.6	811	9	CL673498	CL673498 PRI019c_G
c	29	44.4	16.6	820	9	CL668273	CL668273 AW948147
c	30	44.2	16.5	643	2	AW948147	AW948147 RC0-MT001
	31	44	16.5	381	1	AU180248	AU180248 AU180248
c	32	44	16.5	814	7	CN586292	CN586292 USDA-FP_1
c	33	43.8	16.4	1101	8	AF029514	AF029514 AF029514
	34	43.6	16.3	351	1	AI903023	AI903023 QV-BT022-
c	35	43.2	16.2	1197	8	BZ579062	BZ579062 msh2 6160
c	36	43	16.1	343	2	BI895648	BI895648 EtESTeb01
	37	42.6	16.0	330	2	BE092318	BE092318 IL2-BT073
c	38	42.6	16.0	694	2	AW948136	AW948136 RC0-MT001
c	39	42.6	16.0	730	2	AW948130	AW948130 RC0-MT001
c	40	42.4	16.0	738	2	AW948138	AW948138 RC0-MT001
c	41	42.4	15.9	158	2	AW858409	AW858409 CM0-CT034
c	42	42.4	15.9	282	7	CN025695	CN025695 UMC-p4civ
c	43	42.4	15.9	518	5	BX548956	BX548956 BX548956
c	44	42.4	15.9	548	5	BX548957	BX548957 BX548957
c	45	42.4	15.9	791	9	CL670555	CL670555 PRI0162b

ALIGNMENTS

```
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OM nucleic - nucleic search, using sw model

Run on:     April  3, 2005, 20:59:14 ; Search time 168.694 Seconds
                                       (without alignments)
                                       6031.995 Million cell updates/sec

Title:            US-10-088-666-21
Perfect score:    21
Sequence:         1 ccaagtcaacaacgtagttgt 21

Scoring table:    IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched:         4708233 seqs, 2422607955 residues

Total number of hits satisfying chosen parameters:     9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database :        GenEmbl:*
                  1: gb_ba:*
                  2: gb_htg:*
                  3: gb_in:*
                  4: gb_om:*
                  5: gb_ov:*
                  6: gb_pat:*
                  7: gb_ph:*
                  8: gb_pl:*
                  9: gb_pr:*
                 10: gb_ro:*
                 11: gb_sts:*
                 12: gb_sy:*
                 13: gb_un:*
                 14: gb_vi:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	21	100.0	21	6	AX105749	AX105749 Sequence
2	21	100.0	267	6	AX105729	AX105729 Sequence
3	19.4	92.4	657	5	AY666410	AY666410 Troglodyt
4	19.4	92.4	665	5	AY666450	AY666450 Quiscalus
5	19.4	92.4	668	5	AY666444	AY666444 Quiscalus
6	19.4	92.4	668	5	AY666447	AY666447 Dendroica
7	19.4	92.4	687	5	AY666190	AY666190 Geothlypi
8	19.4	92.4	693	5	AY666188	AY666188 Mniotilta
9	19.4	92.4	693	5	AY666299	AY666299 Dendroica
10	19.4	92.4	694	5	AY666186	AY666186 Mniotilta
11	19.4	92.4	694	5	AY666201	AY666201 Geothlypi
12	19.4	92.4	694	5	AY666258	AY666258 Fringilla
13	19.4	92.4	694	5	AY666301	AY666301 Dendroica
14	19.4	92.4	694	5	AY666442	AY666442 Parula am
15	19.4	92.4	694	5	AY665582	AY665582 Dendroica
16	19.4	92.4	4692	5	AY327391	AY327391 Basileute
17	19.4	92.4	4692	5	AY327393	AY327393 Basileute
18	19.4	92.4	4692	5	AY327395	AY327395 Basileute
19	19.4	92.4	4692	5	AY327396	AY327396 Basileute
20	19.4	92.4	4692	5	AY327398	AY327398 Basileute
21	19.4	92.4	4693	5	AY327394	AY327394 Basileute
22	19.4	92.4	4693	5	AY327399	AY327399 Basileute
23	19.4	92.4	4693	5	AY327400	AY327400 Basileute
24	19.4	92.4	4693	5	AY327401	AY327401 Basileute
25	19.4	92.4	4694	5	AY327397	AY327397 Basileute
26	19.4	92.4	4695	5	AY327392	AY327392 Basileute
27	19.4	92.4	4696	5	AY327389	AY327389 Dendroica
28	18.4	87.6	666	5	AY666470	AY666470 Troglodyt
29	18.4	87.6	694	5	AY666367	AY666367 Molothrus
30	18.4	87.6	694	5	AY666368	AY666368 Molothrus
31	18	85.7	2215	3 c	CVU89789	U89789 Calliphora
32	17.8	84.8	384	5	AY275856	AY275856 Coeligena
33	17.8	84.8	618	5	AY666465	AY666465 Dendroica
34	17.8	84.8	656	5	AY666420	AY666420 Vermivora
35	17.8	84.8	657	5	AY666215	AY666215 Anthus ru
36	17.8	84.8	659	5	AY666511	AY666511 Piranga o
37	17.8	84.8	660	5	AY666204	AY666204 Setophaga
38	17.8	84.8	662	5	AY666455	AY666455 Dolichony
39	17.8	84.8	663	5	AY666423	AY666423 Cardinali
40	17.8	84.8	665	5	AY666389	AY666389 Oenanthe
41	17.8	84.8	666	5	AY666584	AY666584 Wilsonia
42	17.8	84.8	667	5	AY666516	AY666516 Sturnella
43	17.8	84.8	668	5	AY666545	AY666545 Vermivora
44	17.8	84.8	668	5	AY666566	AY666566 Icterus g
45	17.8	84.8	670	5	AY666453	AY666453 Dendroica

ALIGNMENTS

```
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OM nucleic - nucleic search, using sw model

Run on:        April  3, 2005, 20:53:24 ; Search time 72.8378 Seconds
                                          (without alignments)
                                          1706.731 Million cell updates/sec

Title:         US-10-088-666-21
Perfect score: 21
Sequence:      1 ccaagtcaacaacgtagtgt 21

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched:      439206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters:   8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     N_Geneseq_16Dec04:*
            1: geneseqn1980s:*
            2: geneseqn1990s:*
            3: geneseqn2000s:*
            4: geneseqn2001as:*
            5: geneseqn2001bs:*
            6: geneseqn2002as:*
            7: geneseqn2002bs:*
            8: geneseqn2003as:*
            9: geneseqn2003bs:*
           10: geneseqn2003cs:*
           11: geneseqn2003ds:*
           12: geneseqn2004as:*
           13: geneseqn2004bs:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Query Length	DB	ID	Description
1		21	100.0	21	5	AAF61586	Aaf61586 Lactobaci
2		21	100.0	267	5	AAF61566	Aaf61566 Lactobaci
3	c	18	85.7	2215	3	AAZ43884	Aaz43884 C. vicina
4		17.8	84.8	207	8	ABX39064	Abx39064 Bovine ES
5		17.8	84.8	211	8	ABX36896	Abx36896 Bovine ES
6		17.8	84.8	229	8	ABX39055	Abx39055 Bovine ES
7		17.8	84.8	239	8	ABX48286	Abx48286 Bovine ES
8		17.8	84.8	242	8	ABX37833	Abx37833 Bovine ES
9		17.8	84.8	247	8	ABX35018	Abx35018 Bovine ES
10		17.8	84.8	292	8	ABX42572	Abx42572 Bovine ES
11		17.8	84.8	301	8	ABX34921	Abx34921 Bovine ES
12	c	17.8	84.8	308	8	ABX45227	Abx45227 Bovine ES
13		17.8	84.8	340	8	ABX37596	Abx37596 Bovine ES
14		17.8	84.8	341	8	ABX37026	Abx37026 Bovine ES
15		17.8	84.8	342	8	ABX46317	Abx46317 Bovine ES
16		17.8	84.8	348	8	ABX44238	Abx44238 Bovine ES
17		17.8	84.8	358	8	ABX43307	Abx43307 Bovine ES
18		17.8	84.8	360	8	ABX36914	Abx36914 Bovine ES
19		17.8	84.8	360	8	ABX47692	Abx47692 Bovine ES
20		17.8	84.8	366	8	ABX43494	Abx43494 Bovine ES
21		17.8	84.8	366	8	ABX48929	Abx48929 Bovine ES
22		17.8	84.8	368	8	ABX39058	Abx39058 Bovine ES
23		17.8	84.8	378	8	ABX37801	Abx37801 Bovine ES
24		17.8	84.8	382	8	ABX35050	Abx35050 Bovine ES
25		17.8	84.8	385	8	ABX45476	Abx45476 Bovine ES
26		17.8	84.8	391	8	ABX45410	Abx45410 Bovine ES
27		17.8	84.8	395	8	ABX37340	Abx37340 Bovine ES
28		17.8	84.8	398	8	ABX41848	Abx41848 Bovine ES
29		17.8	84.8	399	8	ABX44231	Abx44231 Bovine ES
30		17.8	84.8	404	8	ABX35014	Abx35014 Bovine ES
31		17.8	84.8	404	8	ABX37630	Abx37630 Bovine ES
32		17.8	84.8	405	8	ABX42081	Abx42081 Bovine ES
33		17.8	84.8	406	8	ABX47215	Abx47215 Bovine ES
34		17.8	84.8	407	8	ABX44681	Abx44681 Bovine ES
35		17.8	84.8	416	8	ABX46352	Abx46352 Bovine ES
36		17.8	84.8	417	8	ABX44888	Abx44888 Bovine ES
37		17.8	84.8	419	8	ABX42344	Abx42344 Bovine ES
38		17.8	84.8	420	8	ABX40952	Abx40952 Bovine ES
39		17.8	84.8	427	8	ABX42638	Abx42638 Bovine ES
40		17.8	84.8	430	8	ABX40746	Abx40746 Bovine ES
41		17.8	84.8	458	8	ABX43980	Abx43980 Bovine ES
42		17.8	84.8	553	6	ABN73905	Abn73905 Bovine em
43		17.8	84.8	586	6	ABN73190	Abn73190 Bovine em
44		17.8	84.8	606	6	ABN73809	Abn73809 Bovine em
45		17.8	84.8	641	6	ABN73340	Abn73340 Bovine em

GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: April 3, 2005, 22:12:40 ; Search time 21.3153 Seconds
                                          (without alignments)
                                          1612.071 Million cell updates/sec

Title: US-10-088-666-21
Perfect score: 21
Sequence: 1 ccaagtcaacaacgtagtgt 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued Patents NA:*
               1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
               2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
               3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
               4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
               5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
               6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1	c	16.8	80.0	601	4	US-09-949-016-27938	Sequence 27938, A
2	c	16.8	80.0	601	4	US-09-949-016-128821	Sequence 128821,
3	c	16.8	80.0	59977	4	US-09-949-016-12259	Sequence 12259, A
4	c	16.8	80.0	59978	4	US-09-949-016-15397	Sequence 15397, A
5		16.4	78.1	422592	4	US-09-949-016-14182	Sequence 14182, A
6		16.2	77.1	525	4	US-09-248-796A-1527	Sequence 1527, Ap
7		16.2	77.1	963	4	US-09-328-352-3811	Sequence 3811, Ap
8		16.2	77.1	8878	1	US-08-759-444-2	Sequence 2, Appli
9		16.2	77.1	9880	3	US-08-680-897-1	Sequence 1, Appli
10		15.8	75.2	996	3	US-09-094-557-33	Sequence 33, Appl
11	c	15.8	75.2	1050	3	US-09-134-000C-2255	Sequence 2255, Ap
12	c	15.8	75.2	1053	3	US-09-071-035-409	Sequence 409, App
13	c	15.8	73.3	2666	4	US-09-524-101D-21	Sequence 21, Appl
14	c	15.4	73.3	780	4	US-09-248-796A-6461	Sequence 6461, Ap
15	c	15.4	73.3	1380	4	US-09-328-352-537	Sequence 537, App
16	c	15.4	73.3	68778	4	US-09-949-016-16406	Sequence 16406, A
17	c	15.2	72.4	601	4	US-09-949-016-39292	Sequence 39292, A
18	c	15.2	72.4	601	4	US-09-949-016-76309	Sequence 76309, A
19		15.2	72.4	735	4	US-09-248-796A-6839	Sequence 6839, Ap
20		15.2	72.4	1610	3	US-09-059-769-19	Sequence 19, Appl
21	c	15.2	72.4	2209	4	US-09-489-847-16	Sequence 16, Appl
22	c	15.2	72.4	2535	4	US-09-949-016-2216	Sequence 2216, Ap
23	c	15.2	72.4	2565	4	US-09-949-016-1092	Sequence 1092, Ap
24	c	15.2	72.4	3070	4	US-09-799-451-652	Sequence 652, App
25		15.2	72.4	4326	4	US-09-949-016-676	Sequence 676, App
26		15.2	72.4	5015	4	US-09-949-016-12884	Sequence 12884, A
27	c	15.2	72.4	6536	4	US-09-949-016-13958	Sequence 13958, A
28	c	15.2	72.4	6538	4	US-09-949-016-12834	Sequence 12834, A
29		15.2	72.4	12802	4	US-09-949-016-11792	Sequence 11792, A
30		15.2	72.4	13508	4	US-08-956-171E-120	Sequence 120, App
31		15.2	72.4	13508	4	US-08-781-986A-120	Sequence 120, App
32	c	15.2	72.4	22374	4	US-09-949-016-14938	Sequence 14938, A
33		15.2	72.4	47363	4	US-09-949-016-13420	Sequence 13420, A
34	c	15.2	72.4	142783	4	US-09-949-016-15127	Sequence 15127, A
35		15.2	72.4	192956	4	US-09-949-016-14382	Sequence 14382, A
36	c	15.2	72.4	317366	4	US-09-949-016-16001	Sequence 16001, A
37		15.2	72.4	393753	4	US-09-949-016-14573	Sequence 14573, A
38		15.2	72.4	393753	4	US-09-949-016-14574	Sequence 14574, A
39		15.2	72.4	450395	4	US-09-949-016-15473	Sequence 15473, A
40		15.2	72.4	818128	4	US-09-949-016-14546	Sequence 14546, A
41		15.2	72.4	818128	4	US-09-949-016-14547	Sequence 14547, A
42		15.2	72.4	818128	4	US-09-949-016-14548	Sequence 14548, A
43		15.2	72.4	818128	4	US-09-949-016-14549	Sequence 14549, A
44		15.2	72.4	818128	4	US-09-949-016-14550	Sequence 14550, A
45		15.2	72.4	818128	4	US-09-949-016-14551	Sequence 14551, A

ALIGNMENTS

RESULT 1
US-09-949-016-27938/c
; Sequence 27938, Application US/0994916

OM nucleic - nucleic search, using sw model

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GenCore version 5.1.6

Run on: April 3, 2005, 23:20:50 ; Search time 469.757 seconds
(without alignments)
270.571 Million cell updates/sec

Title: US-10-088-666-21
Perfect score: 21
Sequence: 1 ccaagtcaacaacgtagtgt 21

Scoring table: IDENTITY.NUC
Gapop 10.0 , Gapext 1.0

Searched: 5607317 seqs, 302624599 residues

Total number of hits satisfying chosen parameters: 11214634

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match *	Length	DB	ID	Description
1	17.8	84.8	207	9	US-09-960-352-4229	Sequence 4229, Ap
2	17.8	84.8	211	9	US-09-960-352-2061	Sequence 2061, Ap
3	17.8	84.8	229	9	US-09-960-352-4220	Sequence 4220, Ap
4	17.8	84.8	239	9	US-09-960-352-13451	Sequence 13451, A
5	17.8	84.8	242	9	US-09-960-352-2998	Sequence 2998, Ap
6	17.8	84.8	247	9	US-09-960-352-183	Sequence 183, App
7	17.8	84.8	292	9	US-09-960-352-7737	Sequence 7737, Ap
c 8	17.8	84.8	301	9	US-09-960-352-86	Sequence 86, Appl
9	17.8	84.8	308	9	US-09-960-352-10392	Sequence 10392, A
c 10	17.8	84.8	340	9	US-09-960-352-2761	Sequence 2761, Ap
11	17.8	84.8	341	9	US-09-960-352-2191	Sequence 2191, Ap
12	17.8	84.8	342	9	US-09-960-352-11482	Sequence 11482, A
13	17.8	84.8	348	9	US-09-960-352-9403	Sequence 9403, Ap
14	17.8	84.8	358	9	US-09-960-352-8472	Sequence 8472, Ap
15	17.8	84.8	360	9	US-09-960-352-2079	Sequence 2079, Ap
16	17.8	84.8	360	9	US-09-960-352-12857	Sequence 12857, A
17	17.8	84.8	366	9	US-09-960-352-8659	Sequence 8659, Ap
18	17.8	84.8	366	9	US-09-960-352-14094	Sequence 14094, A
19	17.8	84.8	368	9	US-09-960-352-4223	Sequence 4223, Ap
20	17.8	84.8	378	9	US-09-960-352-2966	Sequence 2966, Ap
21	17.8	84.8	382	9	US-09-960-352-215	Sequence 215, App
22	17.8	84.8	385	9	US-09-960-352-10641	Sequence 10641, A
23	17.8	84.8	391	9	US-09-960-352-10595	Sequence 10595, A
24	17.8	84.8	395	9	US-09-960-352-2505	Sequence 2505, Ap
25	17.8	84.8	398	9	US-09-960-352-7013	Sequence 7013, Ap
26	17.8	84.8	399	9	US-09-960-352-9396	Sequence 9396, Ap
27	17.8	84.8	404	9	US-09-960-352-179	Sequence 179, App
28	17.8	84.8	404	9	US-09-960-352-2795	Sequence 2795, Ap
29	17.8	84.8	405	9	US-09-960-352-7246	Sequence 7246, Ap
30	17.8	84.8	406	9	US-09-960-352-12380	Sequence 12380, A
31	17.8	84.8	407	9	US-09-960-352-9846	Sequence 9846, Ap
32	17.8	84.8	416	9	US-09-960-352-11517	Sequence 11517, A
33	17.8	84.8	417	9	US-09-960-352-10053	Sequence 10053, A
34	17.8	84.8	419	9	US-09-960-352-7509	Sequence 7509, Ap
35	17.8	84.8	420	9	US-09-960-352-6117	Sequence 6117, Ap
36	17.8	84.8	427	9	US-09-960-352-7803	Sequence 7803, Ap
37	17.8	84.8	430	9	US-09-960-352-5911	Sequence 5911, Ap
38	17.8	84.8	458	9	US-09-960-352-9145	Sequence 9145, Ap
39	17.8	84.8	553	11	US-09-876-143-840	Sequence 840, App
40	17.8	84.8	586	11	US-09-876-143-140	Sequence 140, App
41	17.8	84.8	606	11	US-09-876-143-744	Sequence 744, App
42	17.8	84.8	641	11	US-09-876-143-197	Sequence 197, App
43	17.8	84.8	641	11	US-09-876-143-285	Sequence 285, App
44	17.8	84.8	690	11	US-09-876-143-791	Sequence 791, App
45	17.8	84.8	957	11	US-09-876-143-1436	Sequence 1436, Ap

ALIGNMENTS

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                GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:    April  3, 2005, 22:11:20 ; Search time 627.919 Seconds
                                      (without alignments)
                                      1273.014 Million cell updates/sec

Title:           US-10-088-666-21
Perfect score:   21
Sequence:        1 ccaagtcaacaacgtagttgt 21

Scoring table:   IDENTITY_NUC
                 Gapop 10.0, Gapext 1.0

Searched:        34239544 seqs, 1903214700 residues

Total number of hits satisfying chosen parameters:    68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :

        EST:*
          1: gb_est1:*
          2: gb_est2:*
          3: gb_htc:*
          4: gb_est3:*
          5: gb_est4:*
          6: gb_est5:*
          7: gb_est6:*
          8: gb_gss1:*
          9: gb_gss2:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Match	Query Match Length	DB	ID	Description
	1	18	85.7	779	8	BH542735	BH542735 BOGXU95TR
	2	17.8	84.8	197	2	BF430206	BF430206 256171 MA
	3	17.8	84.8	204	2	BE477537	BE477537 161290 BA
	4	17.8	84.8	214	2	BE478105	BE478105 162195 BA
	5	17.8	84.8	218	2	BE486429	BE486429 174324 BA
	6	17.8	84.8	261	7	CR383046	CR383046 CR383046
	7	17.8	84.8	275	7	CO883254	CO883254 BovGen_11
	8	17.8	84.8	290	7	CF614527	CF614527 CES008733
	9	17.8	84.8	313	2	AW426583	AW426583 60977 MAR
c	10	17.8	84.8	337	5	BQ640947	BQ640947 SSH-Bbb1c
	11	17.8	84.8	369	2	BE483687	BE483687 169949 BA
	12	17.8	84.8	387	2	BE476991	BE476991 160485 BA
	13	17.8	84.8	401	2	CV089879	CV089879 SnESTbaa3
	14	17.8	84.8	413	1	AV613476	AV613476 AV613476
c	15	17.8	84.8	418	7	CF362784	CF362784 830575 MA
c	16	17.8	84.8	420	6	CB168898	CB168898 CWI602769
	17	17.8	84.8	421	2	BF230248	BF230248 251764 BA
	18	17.8	84.8	424	2	BE588467	BE588467 193965 BA
	19	17.8	84.8	427	1	AV618453	AV618453 AV618453
c	20	17.8	84.8	432	6	CB166949	CB166949 BTU602600
	21	17.8	84.8	442	2	BE476579	BE476579 159906 BA
	22	17.8	84.8	450	2	BE483083	BE483083 169114 BA
	23	17.8	84.8	451	4	BM432873	BM432873 1JEJ7C4.a
	24	17.8	84.8	451	5	BP110601	BP110601 BP110601
	25	17.8	84.8	454	6	CB221784	CB221784 1IL19H7 B
	26	17.8	84.8	471	2	BE487090	BE487090 175658 BA
	27	17.8	84.8	472	2	BE481873	BE481873 167477 BA
	28	17.8	84.8	477	1	AJ691187	AJ691187 AJ691187
	29	17.8	84.8	477	2	BE483952	BE483952 170440 BA
	30	17.8	84.8	479	4	BM431900	BM431900 1JEJ13H12
	31	17.8	84.8	493	2	BE483642	BE483642 169866 BA
	32	17.8	84.8	494	4	BM432022	BM432022 1JEJ15D6.
c	33	17.8	84.8	495	5	BP107620	BP107620 BP107620.
	34	17.8	84.8	498	2	BE481915	BE481915 167527 BA
	35	17.8	84.8	502	2	BE485555	BE485555 172621 BA
	36	17.8	84.8	509	2	BE482287	BE482287 168021 BA
	37	17.8	84.8	512	2	BE481721	BE481721 167202 BA
	38	17.8	84.8	512	2	BE487910	BE487910 177056 BA
	39	17.8	84.8	513	2	BE476202	BE476202 158828 BA
	40	17.8	84.8	513	2	BE480446	BE480446 165528 BA
	41	17.8	84.8	515	1	AV667257	AV667257 AV667257
	42	17.8	84.8	515	7	CF361479	CF361479 827812 MA
	43	17.8	84.8	519	4	BG690664	BG690664 339334 MA
	44	17.8	84.8	522	2	BE481271	BE481271 166655 BA
	45	17.8	84.8	524	5	BP110809	BP110809 BP110809

ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on:        April  3, 2005, 20:59:14 ; Search time 200.826 Seconds
                                          (without alignments)
                                          6031.995 Million cell updates/sec

Title:         US-10-088-666-73
Perfect score: 25
Sequence:      1 tcgagaataattgaataatatcctag 25

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched:      4708233 seqs, 2422607955 residues

Total number of hits satisfying chosen parameters:    9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
             1: gb_ba:*
             2: gb_htg:*
             3: gb_in:*
             4: gb_om:*
             5: gb_ov:*
             6: gb_pat:*
             7: gb_ph:*
             8: gb_pl:*
             9: gb_pr:*
            10: gb_ro:*
            11: gb_sts:*
            12: gb_sy:*
            13: gb_un:*
            14: gb_vi:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	25	100.0	25	6	AX105801	AX105801 Sequence
	2	25	100.0	267	2	AX105729	AX105729 Sequence
c	3	20.4	81.6	110000	2	AC141815_0	AC141815 Apis mell
c	4	20.2	80.8	64701	2	AC079132	AC079132 Homo sapi
c	5	20.2	80.8	178448	2	AC099805	AC099805 Homo sapi
	6	19.8	79.2	153768	2	AC113566	AC113566 Canis fam
	7	19.8	79.2	238427	2	AC113234	AC113234 Canis fam
	8	19.4	77.6	119113	5	BX005199	BX005199 Zebrafish
c	9	19.4	77.6	145011	2	CR548634	CR548634 Danio rer
c	10	19.4	77.6	149163	2	AC073835	AC073835 Homo sapi
	11	19.4	77.6	154412	9	HS144F13	AL035404 Human DNA
	12	19.4	77.6	195130	9	AL359832	AL359832 Human DNA
	13	19.4	77.6	227743	2	CR847529	CR847529 Danio rer
c	14	19.2	76.8	482	11	CR377191	CR377191 Arabidops
c	15	19.2	76.8	1074	10	AY425869	AY425869 Cryptomys
c	16	19.2	76.8	1131	10	AF012235	AF012235 Cryptomys
c	17	19.2	76.8	35291	5	BX649551	BX649551 Zebrafish
	18	19.2	76.8	83537	5	BX004805	BX004805 Zebrafish
c	19	19.2	76.8	92624	8	AC003000	AC003000 Arabidops
c	20	19.2	76.8	102029	9	AC133537	AC133537 Homo sapi
	21	19.2	76.8	123406	8	AC120508	AC120508 Oryza sat
	22	19.2	76.8	134184	2	AC150028	AC150028 Canis fam
c	23	19.2	76.8	135129	2	AC148864	AC148864 Canis fam
	24	19.2	76.8	137923	5	BX640536	BX640536 Zebrafish
c	25	19.2	76.8	152841	2	AL929463	AL929463 Danio rer
c	26	19.2	76.8	153438	2	AC117959	AC117959 Rattus no
	27	19.2	76.8	174846	2	AC141676	AC141676 Apis mell
	28	19.2	76.8	177722	2	BX928747	BX928747 Danio rer
	29	19.2	76.8	189219	9	AC092982	AC092982 Homo sapi
c	30	19.2	76.8	189355	9	AC053539	AC053539 Homo sapi
	31	19.2	76.8	194717	9	AC113424	AC113424 Homo sapi
c	32	19.2	76.8	202587	2	AC119862	AC119862 Mus muscu
	33	19.2	76.8	202922	2	BX901959	BX901959 Danio rer
c	34	19.2	76.8	222615	2	AL929345	AL929345 Zebrafish
	35	19.2	76.8	226614	2	BX957306	BX957306 Danio rer
c	36	19.2	76.8	268324	5	AL954838	AL954838 Zebrafish
	37	19.2	76.8	342116	2	AC130918	AC130918 Rattus no
	38	19.2	76.8	348465	2	AC131165	AC131165 Rattus no
c	39	19	76.0	164569	2	AC150864	AC150864 Bos tauru
	40	19	76.0	196455	2	AC151118	AC151118 Bos tauru
	41	19	76.0	226341	2	AC130020	AC130020 Rattus no
	42	18.8	75.2	228	6	AX566136	AX566136 Sequence
	43	18.8	75.2	787	3	AY573636	AY573636 Drosophil
	44	18.8	75.2	787	3	AY573639	AY573639 Drosophil
	45	18.8	75.2	788	3	AY573632	AY573632 Drosophil

ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on:    April 3, 2005, 20:53:24 ; Search time 86.7117 Seconds
                                     (without alignments)
                          1706.731 Million cell updates/sec

Title:          US-10-088-666-73
Perfect score:  25
Sequence:       1 tcgagaataattgaataatatctag 25

Scoring table:  IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched:       439206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters:    8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_16Dec04:*
         1:  geneseqn1980s:*
         2:  geneseqn1990s:*
         3:  geneseqn2000s:*
         4:  geneseqn2001aa:*
         5:  geneseqn2001bs:*
         6:  geneseqn2002aa:*
         7:  geneseqn2002bs:*
         8:  geneseqn2003aa:*
         9:  geneseqn2003bs:*
        10:  geneseqn2003cs:*
        11:  geneseqn2003ds:*
        12:  geneseqn2004aa:*
        13:  geneseqn2004bs:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	25	100.0	25	5	AAF61638	Aaf61638 Lactobaci
	2	25	100.0	267	5	AAF61566	Aaf61566 Lactobaci
	3	18.8	75.2	228	8	ABQ82965	Abq82965 Human lun
c	4	18.8	75.2	1324	8	ABQ82966	Abq82966 Human lun
c	5	18.4	73.6	5064	2	AAV69110	Aav69110 Neiserria
	6	18.4	73.6	25426	8	ADA41645	Ada41645 Human sec
	7	18.4	73.6	25426	8	ACC50940	Acc50940 Human sec
	8	18.4	73.6	25426	10	ADD38155	Add38155 cDNA clon
	9	18.4	73.6	25426	10	ADA57777	Ada57777 BAC fragm
	10	18.2	72.8	234	10	ADH82432	Adh82432 Enterococ
c	11	18.2	72.8	332	13	ADS51386	Ads51386 Bacterial
c	12	18.2	72.8	468	10	ADH82431	Adh82431 Enterococ
c	13	18.2	72.8	588	12	ACH72871	Ach72871 Human gen
c	14	18.2	72.8	2179	2	AAX13405	Aax13405 Enterococ
c	15	18.2	72.8	2179	6	ABS99200	Abs99200 Enterococ
c	16	18.2	72.8	22620	4	ABL07500	Abl07500 Drosophil
	17	18.2	72.8	22958	13	ADT05537	Adt05537 Haemophil
	18	18.2	72.8	110000	2	AAT42063_03	Continuation (4 of
c	19	18.2	72.8	163701	13	ABD33351	Abd33351 Murine ca
	20	18.2	72.8	349980	13	ADT05648	Adt05648 Haemophil
c	21	18	72.0	1190	2	AAX13651	Aax13651 Enterococ
c	22	18	72.0	1190	6	ABS99446	Abs99446 Enterococ
	23	18	71.2	5962	10	ABL33286	Abl33286 Human imm
c	24	17.8	71.2	1151	13	ADC08440	Adc08440 Rice DNA
c	25	17.8	71.2	2020	8	ADT05232	Adt05232 Haemophil
	26	17.6	70.4	3393	10	ABT17845	Abt17845 Aspergill
	27	17.6	70.4	103	6	ABX83278	Abx83278 Corn ear-
	28	17.6	70.4	160	10	ABL74381	Abl74381 Corn tass
	29	17.6	70.4	210	10	ABX83795	Abx83795 Corn ear-
	30	17.6	70.4	349	6	ABL83657	Abl83657 Human ova
	31	17.6	70.4	1001	3	AAC57478	Aac57478 Arachidon
	32	17.6	70.4	1001	3	AAC57477	Aac57477 Arachidon
	33	17.6	70.4	1486	3	AAC39081	Aac39081 Arabidops
	34	17.6	70.4	2076	4	ACA33067	Aca33067 Prokaryot
	35	17.6	70.4	2079	4	AAS52961	Aas52961 Enterococ
	36	17.6	70.4	2345	4	ABL22259	Abl22259 Drosophil
	37	17.6	70.4	3212	4	AAV03313	Aav03313 Archaeogl
c	38	17.6	70.4	3212	10	AAL56488	Aal56488 Phosphata
	39	17.6	70.4	5587	4	ABL21402	Abl21402 Drosophil
	40	17.6	70.4	6032	4	AAS63311	Aas63311 Chemicall
c	41	17.6	70.4	8042	4	ABL22258	Abl22258 Drosophil
c	42	17.6	70.4	11429	13	ADS89737	Ads89737 Oligonucl
c	43	17.6	70.4	11429	13	ADS89463	Ads89463 Oligonucl
c	44	17.6	70.4	14429	6	ABL34242	Abl34242 Human imm
c	45	17.6	70.4	14429	6	ABQ67097	Abq67097 Human ang

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                    GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:      April  3, 2005, 22:12:40 ; Search time 25.3754 Seconds
                                        (without alignments)
                                1612.071 Million cell updates/sec

Title:       US-10-088-666-73
Perfect score: 25
Sequence:    1 tcgagaataattgaataatatctag 25

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:    1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters:      2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued Patents NA:*
             1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
             2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
             3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
             4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
             5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
             6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
```

-    Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	19.2	76.8	95566	4	US-09-949-016-11877	Sequence 11877, A
c 2	18.8	75.2	236964	4	US-09-949-016-15753	Sequence 15753, A
c 3	18.6	74.4	211049	4	US-09-949-016-15770	Sequence 15770, A
c 4	18.4	73.6	5064	3	US-08-936-107A-8	Sequence 8, Appli
5	18.4	73.6	34628	4	US-09-949-016-12304	Sequence 12304, A
6	18.4	73.6	34779	4	US-09-944-016-13787	Sequence 13787, A
7	18.2	72.8	234	4	US-09-313-294A-1738	Sequence 317, App
c 8	18.2	72.8	468	4	US-09-134-000C-316	Sequence 316, App
9	18.2	72.8	210	4	US-09-949-016-14143	Sequence 14143, A
10	18.2	72.8	143550	4	US-09-557-884-1	Sequence 1, Appli
11	18.2	72.8	1830121	4	US-09-643-990A-1	Sequence 1, Appli
c 12	17.8	71.2	601	4	US-09-949-016-166500	Sequence 166500, A
c 13	17.8	71.2	30054	4	US-09-949-016-16429	Sequence 16429, A
c 14	17.8	71.2	35122	4	US-09-949-016-11873	Sequence 11873, A
c 15	17.8	71.2	157644	4	US-09-949-016-16179	Sequence 16179, A
c 16	17.8	71.2	157644	4	US-09-949-016-16180	Sequence 16180, A
17	17.6	70.4	103	4	US-09-313-294A-1738	Sequence 1738, Ap
18	17.6	70.4	210	4	US-09-313-294A-2255	Sequence 2255, Ap
19	17.6	70.4	1001	3	US-09-641-638-111	Sequence 111, App
20	17.6	70.4	1001	3	US-09-641-638-112	Sequence 112, App
21	17.6	70.4	1001	4	US-10-170-097-111	Sequence 111, App
22	17.6	70.4	1001	4	US-10-170-097-112	Sequence 112, App
23	17.6	70.4	27270	4	US-09-949-016-13822	Sequence 13822, A
24	17.4	69.6	25227	4	US-09-949-016-11847	Sequence 11847, A
25	17.4	69.6	25227	4	US-09-949-016-14863	Sequence 14863, A
26	17.4	69.6	149543	4	US-09-949-016-15947	Sequence 15947, A
c 27	17.4	69.6	1830121	4	US-09-557-884-1	Sequence 1, Appli
c 28	17.4	69.6	1830121	4	US-09-643-990A-1	Sequence 1, Appli
29	17.2	68.8	441	4	US-09-710-279-1795	Sequence 1795, Ap
30	17.2	68.8	462	3	US-09-134-001C-2294	Sequence 2294, Ap
c 31	17.2	68.8	467	4	US-09-640-211A-1667	Sequence 1667, Ap
c 32	17.2	68.8	473	4	US-09-640-211A-1740	Sequence 1740, Ap
c 33	17.2	68.8	533	4	US-09-640-211A-1804	Sequence 1804, Ap
c 34	17.2	68.8	563	4	US-09-640-211A-1662	Sequence 1662, Ap
35	17.2	68.8	601	4	US-09-949-016-186599	Sequence 186599,
c 36	17.2	68.8	601	4	US-09-949-016-186600	Sequence 186600,
37	17.2	68.8	2943	4	US-09-710-279-3983	Sequence 3983, Ap
c 38	17.2	68.8	3249	4	US-09-710-279-3622	Sequence 3622, Ap
39	17.2	68.8	3442	4	US-09-710-279-4030	Sequence 4030, Ap
40	17.2	68.8	10449	4	US-09-949-016-14475	Sequence 14475, A
c 41	17.2	68.8	140725	4	US-09-949-016-17074	Sequence 17074, A
c 42	17.2	68.8	363032	4	US-09-949-016-12415	Sequence 12415, A
c 43	17.2	68.8	363033	4	US-09-949-016-15754	Sequence 15754, A
c 44	17	68.0	601	4	US-09-949-016-63288	Sequence 63288, A
45	17	68.0	601	4	US-09-949-016-125488	Sequence 125488,

ALIGNMENTS

```
RESULT 1
US-09-949-016-11877
; Sequence 11877, Application US/0994916
```

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              GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:   April  3, 2005, 23:20:50 ; Search time 559.234 Seconds
                                       (without alignments)
                                      270.571 Million cell updates/sec

Title:         US-10-088-666-73
Perfect score: 25
Sequence:      1 tcgagaataattgaataatactctag 25

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched:      5607317 seqs, 302624599 residues

Total number of hits satisfying chosen parameters:    11214634

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  Published_Applications_NA:*
      1:  /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
      2:  /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
      3:  /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
      4:  /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
      5:  /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
      6:  /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
      7:  /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
      8:  /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
      9:  /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
     10:  /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
     11:  /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
     12:  /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
     13:  /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
     14:  /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
     15:  /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
     16:  /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
     17:  /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
     18:  /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
     19:  /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
     20:  /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
     21:  /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
     22:  /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
```

SUMMARIES

	Result No.	Score	Query Match	Length	DB	ID	Description
	1	18.8	75.2	228	14	US-10-016-349A-108	Sequence 108, App
	2	18.8	75.2	1324	14	US-10-016-349A-109	Sequence 109, App
c	3	18.6	74.4	1206	18	US-10-425-115-119404	Sequence 119404,
c	4	18.4	73.6	1891	18	US-10-437-963-45894	Sequence 45894, A
c	5	18.2	72.8	332	17	US-10-369-493-29816	Sequence 29816, A
c	6	18.2	72.8	588	16	US-10-029-386-6066	Sequence 6066, Ap
c	7	18.2	72.8	638	18	US-10-767-701-26220	Sequence 26220, A
c	8	18.2	72.8	2179	9	US-09-070-927A-468	Sequence 468, App
c	9	18.2	72.8	163701	18	US-10-322-281-439	Sequence 439, Appl
	10	18.2	72.8	1830121	17	US-10-329-670-1	Sequence 1, Appli
	11	18.2	72.8	1830121	18	US-10-158-865-1	Sequence 1, Appli
c	12	18	72.0	1190	9	US-09-070-927A-714	Sequence 714, App
	13	18	72.0	5962	15	US-10-311-455-1259	Sequence 1259, Ap
c	14	17.8	71.2	493	17	US-10-424-599-74009	Sequence 74009, A
	15	17.8	71.2	1118	13	US-10-027-632-118527	Sequence 118527,
	16	17.8	71.2	1118	13	US-10-027-632-118528	Sequence 118528,
	17	17.8	71.2	1118	17	US-10-027-632-118527	Sequence 118527,
	18	17.8	71.2	1118	17	US-10-027-632-118528	Sequence 118528,
c	19	17.8	71.2	1710	19	US-10-662-126-26	Sequence 26, Appl
c	20	17.8	71.2	3393	15	US-10-128-714-203	Sequence 203, App
	21	17.6	70.4	160	9	US-09-294-093B-3755	Sequence 3755, Ap
c	22	17.6	70.4	204	18	US-10-425-115-36493	Sequence 36493, A
c	23	17.6	70.4	332	18	US-10-425-115-104351	Sequence 104351,
	24	17.6	70.4	349	9	US-09-867-701-6635	Sequence 6635, Ap
c	25	17.6	70.4	578	17	US-10-425-114-34850	Sequence 34850, A
c	26	17.6	70.4	601	13	US-10-027-632-18543	Sequence 18543, A
	27	17.6	70.4	601	17	US-10-027-632-18543	Sequence 18543, A
c	28	17.6	70.4	615	13	US-10-027-632-282529	Sequence 282529,
c	29	17.6	70.4	615	13	US-10-027-632-282529	Sequence 282529,
	30	17.6	70.4	771	17	US-10-425-114-1795	Sequence 1795, Ap
	31	17.6	70.4	998	17	US-10-425-114-19489	Sequence 11489, A
	32	17.6	70.4	1001	17	US-10-170-097-111	Sequence 111, App
	33	17.6	70.4	1001	17	US-10-170-097-112	Sequence 112, App
	34	17.6	70.4	1001	19	US-10-926-684-111	Sequence 111, App
	35	17.6	70.4	1001	19	US-10-926-684-112	Sequence 112, App
	36	17.6	70.4	1141	17	US-10-425-114-712	Sequence 712, App
	37	17.6	70.4	1163	17	US-10-425-114-19232	Sequence 19232, A
	38	17.6	70.4	1298	17	US-10-425-114-6794	Sequence 6794, Ap
	39	17.6	70.4	1298	18	US-10-425-115-90866	Sequence 90866, A
	40	17.6	70.4	1359	17	US-10-424-599-35445	Sequence 35445, A
	41	17.6	70.4	1370	17	US-10-425-114-1104	Sequence 1104, Ap
	42	17.6	70.4	1375	17	US-10-425-114-5129	Sequence 5129, Ap
	43	17.6	70.4	1388	17	US-10-425-114-1028	Sequence 1028, Ap
	44	17.6	70.4	1388	17	US-10-425-114-3166	Sequence 3166, Ap
	45	17.6	70.4	1389	17	US-10-425-114-15767	Sequence 15767, A

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
US-10-016-349A-108

OM nucleic - nucleic search, using sw model

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                    GenCore version 5.1.6
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Run on: April 3, 2005, 22:11:20 ; Search time 747.523 Seconds
                                          (without alignments)
                                          1273.014 Million cell updates/sec

Title: US-10-088-666-73
Perfect score: 25
Sequence: 1 tcgagaataattgaataatatcctag 25
Scoring table: IDENTITY_NUC
                   Gapop 10.0 , Gapext 1.0

Searched: 3423544 seqs, 1903213700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
              1: gb_est1:*
              2: gb_est2:*
              3: gb_htc:*
              4: gb_est3:*
              5: gb_est4:*
              6: gb_est5:*
              7: gb_est6:*
              8: gb_gss1:*
              9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	20.8	83.2	717	9	AG296763	AG296763 Mus muscu
c 2	20.2	80.8	460	9	AQ489622	AQ489622 RPCI-11-2
c 3	19.8	79.2	887	9	CNS06W55	AL417999 T3 end of
c 4	19.4	77.6	622	9	CL350164	CL350164 RPCI44_31
5	19.4	77.6	848	8	AZ683885	AZ683885 ENTLp32TF
6	19.4	77.6	877	8	CC141515	CC141515 NDL.32K2.
7	19.4	77.6	898	8	BH133066	BH133066 ENTPC66TR
8	19.4	77.6	900	8	BH147215	BH147215 ENTOP41TR
9	19.4	77.6	903	8	BH136872	BH136872 ENTNA82TR
10	19.2	76.8	214	9	CR398469	CR398469 Arabidops
11	19.2	76.8	277	9	CG148828	CG148828 PUFKV46TB
12	19.2	76.8	307	9	CL257264	CL257264 ZMMBBb061
13	19.2	76.8	340	6	CD324627	CD324627 StrPu537.
14	19.2	76.8	382	9	CE401158	CE401158 tigr-gss-
15	19.2	76.8	386	9	CE624663	CE624663 tigr-gss-
16	19.2	76.8	390	8	BZ632366	BZ632366 PUABA54TD
17	19.2	76.8	405	9	CG148831	CG148831 PUFKV46TD
18	19.2	76.8	409	8	BZ632406	BZ632406 PUAAT41TB
19	19.2	76.8	413	8	BZ632362	BZ632362 PUABA54TB
c 20	19.2	76.8	418	8	BZ632408	BZ632408 PUAAT41TD
21	19.2	76.8	424	8	BH170927	BH170927 SALK_0035
22	19.2	76.8	464	7	CE853568	CE853568 tigr-gss-
23	19.2	76.8	482	7	CO517136	CO517136 sl3dSG29H
c 24	19.2	76.8	568	9	CE345622	CE345622 tigr-gss-
c 25	19.2	76.8	570	9	CE313026	CE313026 tigr-gss-
c 26	19.2	76.8	583	9	CE029479	CE029479 tigr-gss-
c 27	19.2	76.8	601	9	CE378676	CE378676 tigr-gss-
28	19.2	76.8	630	9	CE407289	CE407289 tigr-gss-
c 29	19.2	76.8	639	9	CE397029	CE397029 tigr-gss-
30	19.2	76.8	641	9	CL379696	CL379696 RPCI44_42
31	19.2	76.8	646	9	CE717195	CE717195 tigr-gss-
c 32	19.2	76.8	685	9	CE745651	CE745651 tigr-gss-
c 33	19.2	76.8	709	9	CL827541	CL827541 OR_CBa004
c 34	19.2	76.8	711	9	AG123355	AG123355 Pan_trog1
35	19.2	76.8	713	9	CE459772	CE459772 tigr-gss-
c 36	19.2	76.8	742	9	CE224657	CE224657 tigr-gss-
37	19.2	76.8	757	9	CL757754	CL757754 OR_BBa012
c 38	19.2	76.8	791	9	CL929820	CL929820 OA_ABa003
c 39	19.2	76.8	833	9	CG048515	CG048515 PUILQ60TB
c 40	19.2	76.8	911	8	BZ829021	BZ829021 PUGBQ27TD
41	19	76.0	888	8	CG965204	CG965204 MBEMD88TF
c 42	18.8	75.2	402	8	AQ207867	AQ207867 HS_3138_A
43	18.8	75.2	405	1	AI872073	AI872073 tz6lg11_x
44	18.8	75.2	506	9	CG696733	CG696733 MUGQ_CH25
45	18.8	75.2	574	8	AQ466749	AQ466749 HS_5170_A

ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on:    April  3, 2005, 20:59:14 ; Search time 160.661 Seconds
                                       (without alignments)
                                       6031.995 Million cell updates/sec

Title:           US-10-088-666-74
Perfect score:   20
Sequence:        1 gaggaagaagttccttat 20
Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0
Searched:        4708233 seqs, 2422760795 residues
Total number of hits satisfying chosen parameters:   9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
             1: gb_ba:*
             2: gb_htg:*
             3: gb_in:*
             4: gb_om:*
             5: gb_ov:*
             6: gb_pat:*
             7: gb_ph:*
             8: gb_pl:*
             9: gb_pr:*
            10: gb_ro:*
            11: gb_sts:*
            12: gb_sy:*
            13: gb_un:*
            14: gb_vi:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	20	6	AX105802	AX105802 Sequence
	2	20	100.0	267	6	AX105729	AX105729 Sequence
	3	18.4	92.0	337	6	CQ455603	CQ455603 Sequence
	4	18.4	92.0	6076	10	AF272661	AF272661 Rattus no
	5	18.4	92.0	6109	6	AR564346	AR564346 Sequence
	6	18.4	92.0	6109	6	AX239611	AX239611 Sequence
	7	18.4	92.0	6109	10	AF176645	AF176645 Mus muscu
c	8	18.4	92.0	155793	10	AC102821	AC102821 Mus muscu
c	9	18.4	92.0	182757	10	AC122484	AC122484 Mus muscu
c	10	18	90.0	229813	2	AC117613	AC117613 Mus muscu
	11	17.4	87.0	1907	6	CQ723784	CQ723784 Sequence
	12	17.4	87.0	6200	6	AR564347	AR564347 Sequence
	13	17.4	87.0	6200	6	AX239613	AX239613 Sequence
	14	17.4	87.0	6200	9	AF177941	AF177941 Homo sapi
	15	17.4	87.0	6368	6	AX405643	AX405643 Sequence
	16	17.4	87.0	39969	9	HSJ645L19	HSJ645L19 Human DNA
c	17	17.4	87.0	110000	2	AC109525	AC109525 Rattus no
	18	17.4	87.0	157410	2	AC013816	AC013816 Homo sapi
	19	17.4	87.0	166701	2	AC011457	AC011457 Homo sapi
	20	17.4	87.0	166711	9	AC006116	AC006116 Homo sapi
	21	17.4	87.0	168119	5	AC068686	AC068686 Homo sapi
	22	17.4	87.0	169592	2	BX511100	BX511100 Zebrafish
	23	17.4	87.0	175406	2	AC087128	AC087128 Mus muscu
c	24	17.4	87.0	187541	2	AC121560	AC121560 Mus muscu
c	25	17.4	87.0	192944	2	AC146902	AC146902 Callicebu
	26	17.4	87.0	194427	9	AC093153	AC093153 Homo sapi
c	27	17.4	87.0	207004	5	AL954695	AL954695 Zebrafish
	28	17.4	87.0	207596	2	AC141506	AC141506 Rattus no
c	29	17.4	87.0	208657	2	AC046179	AC046179 Homo sapi
	30	17.4	87.0	210636	2	AC105070	AC105070 Mus muscu
	31	17.4	87.0	218244	2	BX571726	BX571726 Danio rer
c	32	17.4	87.0	223843	10	AC102595	AC102595 Mus muscu
c	33	17.4	87.0	229948	2	AC113690	AC113690 Rattus no
	34	17.4	87.0	229563	10	AC024957	AC024957 Mus muscu
c	35	17.4	87.0	235662	2	AC126709	AC126709 Rattus no
	36	17.4	87.0	237019	2	AC094443	AC094443 Rattus no
	37	17.4	87.0	239870	2	AC094970	AC094970 Rattus no
c	38	17.4	87.0	243689	2	AC129281	AC129281 Rattus no
c	39	17.4	87.0	259178	2	AC108971	AC108971 Rattus no
c	40	17.4	87.0	271189	2	AC128515	AC128515 Rattus no
	41	17.4	87.0	304851	2	AC121044	AC121044 Rattus no
	42	17	85.0	101707	2	AC150157	AC150157 Gallus ga
	43	17	85.0	127767	6	CQ868657	CQ868657 Sequence
	44	17	85.0	128809	9	AC021648	AC021648 Homo sapi
c	45	17	85.0	172825	2	AC020614	AC020614 Homo sapi

ALIGNMENTS

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                    GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:    April  3, 2005, 20:53:24 ; Search time 69.3694 Seconds
                                       (without alignments)
                                       1706.731 Million cell updates/sec

Title:           US-10-088-666-74
Perfect score:   20
Sequence:        1 gagggaagaagttccttat 20

Scoring table:   IDENTITY NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        439206 seqs, 295987067 residues

Total number of hits satisfying chosen parameters:     8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       N_Geneseq_16Dec04:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
                 3: geneseqn2000s:*
                 4: geneseqn2001as:*
                 5: geneseqn2001bs:*
                 6: geneseqn2002as:*
                 7: geneseqn2002bs:*
                 8: geneseqn2003as:*
                 9: geneseqn2003bs:*
                 10: geneseqn2003cs:*
                 11: geneseqn2003ds:*
                 12: geneseqn2004as:*
                 13: geneseqn2004bs:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Match	Query Length	DB	ID	Description
1		20	100.0	20	5	AAF61639	Aaf61639 Lactobaci
2		20	100.0	267	5	AAF61566	Aaf61566 Lactobaci
3		18.4	92.0	337	4	ABN26443	Abn26443 Human ORF
4		18.4	92.0	6109	4	AAH78667	Aah78667 Murine Co
5		17.4	87.0	593	12	ACH68151	Ach68151 Human gen
6		17.4	87.0	6159	12	ADQ83504	Adq83504 Human tum
7		17.4	87.0	6200	4	AAH78668	Aah78668 Human COL
8		17.4	87.0	6200	12	ADQ19840	Adq19840 Human sof
9		17.4	87.0	6368	12	ABN59647	Abn59647 Novel hum
10		17.4	87.0	6617	12	ADQ23958	Adq23958 Human sof
11		17	85.0	127767	13	ABD33584	Abd33584 Murine ca
12		17	85.0	127767	13	ADR67023	Adr67023 Mouse can
13	c	16.8	84.0	406	9	ACL23170	Acl23170 DNA clone
14	c	16.8	84.0	514	9	ACL23160	Acl23160 DNA clone
15	c	16.8	84.0	516	9	ACL23162	Acl23162 DNA clone
16	c	16.8	84.0	538	9	ACL23156	Acl23156 DNA clone
17	c	16.8	84.0	548	9	ACL23164	Acl23164 DNA clone
18	c	16.8	84.0	590	9	ACL23143	Acl23143 DNA clone
19	c	16.8	84.0	608	9	ACL23167	Acl23167 DNA clone
20	c	16.8	84.0	617	9	ACL23169	Acl23169 DNA clone
21	c	16.8	84.0	623	9	ACL23148	Acl23148 DNA clone
22	c	16.8	84.0	631	9	ACL23157	Acl23157 DNA clone
23	c	16.8	84.0	637	9	ACL23168	Acl23168 DNA clone
24	c	16.8	84.0	655	9	ACL23158	Acl23158 DNA clone
25	c	16.8	84.0	679	9	ACL23163	Acl23163 DNA clone
26	c	16.8	84.0	681	9	ACL23145	Acl23145 DNA clone
27	c	16.8	84.0	692	9	ACL23161	Acl23161 DNA clone
28	c	16.8	84.0	717	9	ACL23159	Acl23159 DNA clone
29	c	16.8	84.0	722	9	ACL23171	Acl23171 DNA clone
30	c	16.8	84.0	110000	2	AAX91990_04	Continuation (5 of
31	c	16.8	84.0	110000	4	AAK95240_11	Continuation (12 o
32	c	16.8	84.0	110000	4	AAK96733_11	Continuation (12 o
33	c	16.8	84.0	110000	6	ABT00010_11	Continuation (12 o
34	c	16.8	84.0	110000	6	ABT01503_11	Continuation (12 o
35	c	16.8	84.0	110000	12	ADH77486_11	Continuation (12 o
36	c	16.8	84.0	175561	8	AAD55694	Aad55694 Human THB
37	c	16.8	84.0	175561	12	ADL08129	Adl08129 Human gen
38	c	16.8	84.0	273254	3	AAC81914	Aac81914 Chlamydia
39	c	16.4	82.0	255	6	ABK81965	Abk81965 Human dys
40	c	16.4	82.0	465	6	ABK75767	Abk75767 Bacillus
41	c	16.4	82.0	702	6	AAS92053	Aas92053 DNA encod
42	c	16.4	82.0	1340	6	AAD37239	Aad37239 Human dys
43	c	16.4	82.0	1477	12	ADN60337	Adn60337 B. lichen
44	c	16.4	82.0	1667	6	AAD37235	Aad37235 Human dys
45	c	16.4	82.0	1991	6	AAD37231	Aad37231 Human dys

ALIGNMENTS

GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: April 3, 2005, 22:12:40 ; Search time 20.3003 Seconds
(without alignments)
1612.071 Million cell updates/sec

Title: US-10-088-666-74
Perfect score: 20
Sequence: 1 gagggaagaagttcctat 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :   Issued Patents NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/pCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	Query % Match	Match Length	DB	ID	Description
1		18.4	92.0	6109	4	US-09-795-061-1	Sequence 1, Appli
2		17.4	87.0	6200	4	US-09-795-061-3	Sequence 3, Appli
3		16.8	84.0	46319	4	US-09-949-016-12526	Sequence 12526, A
4		16.8	84.0	46323	4	US-09-949-016-13267	Sequence 13267, A
5		16.8	84.0	1230025	4	US-09-198-452A-1	Sequence 1, Appli
6		16.8	84.0	1230230	4	US-09-438-185A-1	Sequence 1, Appli
7		16.4	82.0	5952	3	US-09-687-875A-1	Sequence 1, Appli
8		16.4	82.0	13977	3	US-09-484-970B-60	Sequence 60, Appl
9		15.8	79.0	239	3	US-09-443-184-18	Sequence 18, Appl
10		15.8	79.0	244	3	US-09-443-184-19	Sequence 19, Appl
11		15.8	79.0	267	3	US-09-443-184-17	Sequence 17, Appl
12		15.8	79.0	601	4	US-09-949-016-41020	Sequence 41020, A
13		15.8	79.0	601	4	US-09-949-016-41021	Sequence 41021, A
14		15.8	79.0	601	4	US-09-949-016-44921	Sequence 44921, A
15		15.8	79.0	601	4	US-09-949-016-44922	Sequence 44922, A
16		15.8	79.0	601	4	US-09-949-016-130621	Sequence 130621,
17	c	15.8	79.0	601	4	US-09-949-016-130622	Sequence 130622,
18	c	15.8	79.0	601	4	US-09-949-016-130623	Sequence 130623,
19	c	15.8	79.0	601	4	US-09-949-016-130624	Sequence 130624,
20	c	15.8	79.0	601	4	US-09-949-016-145008	Sequence 145008,
21	c	15.8	79.0	601	4	US-09-949-016-145009	Sequence 145009,
22	c	15.8	79.0	601	4	US-09-949-016-145010	Sequence 145010,
23	c	15.8	79.0	601	4	US-09-949-016-157254	Sequence 157254,
24	c	15.8	79.0	601	4	US-09-949-016-157255	Sequence 157255,
25	c	15.8	79.0	601	4	US-09-949-016-157256	Sequence 157256,
26	c	15.8	79.0	601	4	US-09-949-016-157276	Sequence 157276,
27	c	15.8	79.0	601	4	US-09-949-016-157277	Sequence 157277,
28	c	15.8	79.0	601	4	US-09-949-016-157278	Sequence 157278,
29	c	15.8	79.0	601	4	US-09-949-016-157298	Sequence 157298,
30	c	15.8	79.0	601	4	US-09-949-016-157299	Sequence 157299,
31	c	15.8	79.0	601	4	US-09-949-016-157300	Sequence 157300,
32		15.8	79.0	3001	4	US-09-539-333D-156	Sequence 156, App
33		15.8	79.0	3182	1	US-07-797-556-5	Sequence 5, Appli
34		15.8	79.0	3182	1	US-07-943-843-1	Sequence 1, Appli
35		15.8	79.0	3591	1	US-08-347-003-1	Sequence 1, Appli
36		15.8	79.0	3591	1	US-07-943-843-5	Sequence 5, Appli
37		15.8	79.0	3591	1	US-08-347-003-5	Sequence 5, Appli
38		15.8	79.0	5245	4	US-09-949-016-4210	Sequence 4210, Ap
39		15.8	79.0	5252	4	US-09-949-016-338	Sequence 338, App
40		15.8	79.0	7953	4	US-09-949-016-16886	Sequence 16886, A
41	c	15.8	79.0	25992	4	US-09-949-016-17308	Sequence 17308, A
42	c	15.8	79.0	26000	4	US-09-843-376-10	Sequence 10, Appl
43		15.8	79.0	27632	4	US-09-949-016-12903	Sequence 12903, A
44		15.8	79.0	36456	4	US-09-949-016-12404	Sequence 12404, A
45		15.8	79.0	36457	4	US-09-949-016-13031	Sequence 13031, A

ALIGNMENTS

RESULT 1
US-09-795-061-1
; Sequence 1, Application US/09795061

```
                    GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:    April  3, 2005, 23:20:50 ; Search time 447.387 Seconds
                                       (without alignments)
                                       270.571 Million cell updates/sec

Title:           US-10-088-666-74
Perfect score:   20
Sequence:        1 gaggaagaagtcccttat 20

Scoring table:   IDENTITY NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        5607317 seqs, 302624599 residues

Total number of hits satisfying chosen parameters:      11214634

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    Published_Applications NA:*
          1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
          2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
          3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
          4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
          5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
          6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
          7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
          8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
          9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
         10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
         11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
         12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
         13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
         14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
         15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
         16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
         17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
         18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
         19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
         20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
         21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
         22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%	Query Match Length	DB Length	ID	Description
1	18.4	92.0	6109	10	US-09-795-061-1	Sequence 1, Appli
2	18	90.0	465	18	US-10-425-115-45008	Sequence 45008, A
3	17.4	87.0	593	16	US-10-029-386-1346	Sequence 1346, Ap
4	17.4	87.0	6200	10	US-09-795-061-3	Sequence 3, Appli
5	17.4	87.0	6200	18	US-10-723-860-2659	Sequence 2659, Ap
6	17.4	87.0	6617	18	US-10-723-860-6778	Sequence 6778, Ap
7	17	85.0	127767	18	US-10-322-281-797	Sequence 797, App
c 8	16.8	84.0	175561	14	US-10-017-721-3	Sequence 3, Appli
c 9	16.8	84.0	175561	17	US-10-235-192A-48	Sequence 48, Appl
c 10	16.8	84.0	1230025	17	US-10-289-762-1	Sequence 1, Appli
c 11	16.8	84.0	1503841	9	US-09-795-668-1	Sequence 1, Appli
c 12	16.8	84.0	1503841	9	US-09-795-686-1	Sequence 1, Appli
c 13	16.8	84.0	1503841	19	US-09-946-807-1	Sequence 1, Appli
14	16.4	82.0	25	19	US-10-719-900-626239	Sequence 626239,
15	16.4	82.0	201	18	US-10-719-993-24492	Sequence 24492, A
16	16.4	82.0	255	17	US-10-149-736-7	Sequence 7, Appli
17	16.4	82.0	255	19	US-10-964-536-7	Sequence 7, Appli
18	16.4	82.0	465	9	US-09-974-300-3058	Sequence 3058, Ap
19	16.4	82.0	688	13	US-10-027-632-102170	Sequence 102170,
20	16.4	82.0	688	13	US-10-027-632-102171	Sequence 102171
21	16.4	82.0	688	17	US-10-027-632-102170	Sequence 102170,
22	16.4	82.0	688	17	US-10-027-632-102171	Sequence 102171,
23	16.4	82.0	1340	17	US-09-845-416-11	Sequence 11, Appl
24	16.4	82.0	1667	10	US-09-845-416-7	Sequence 7, Appl
25	16.4	82.0	1991	10	US-09-845-416-3	Sequence 3, Appli
26	16.4	82.0	2022	18	US-10-437-963-57769	Sequence 57769, A
27	16.4	82.0	3446	10	US-09-845-416-14	Sequence 14, Appl
28	16.4	82.0	3510	10	US-09-845-416-12	Sequence 12, Appl
29	16.4	82.0	3531	10	US-09-845-416-10	Sequence 10, Appl
30	16.4	82.0	3858	10	US-09-845-416-9	Sequence 9, Appli
31	16.4	82.0	3999	10	US-09-845-416-6	Sequence 6, Appli
32	16.4	82.0	4182	10	US-09-845-416-2	Sequence 2, Appli
33	16.4	82.0	4414	10	US-09-845-416-32	Sequence 32, Appl
34	16.4	82.0	4476	10	US-09-845-416-31	Sequence 31, Appl
35	16.4	82.0	4498	10	US-09-845-416-30	Sequence 30, Appl
36	16.4	82.0	4825	10	US-09-845-416-29	Sequence 29, Appl
37	16.4	82.0	4848	10	US-09-845-416-35	Sequence 35, Appl
38	16.4	82.0	4966	10	US-09-845-416-28	Sequence 28, Appl
39	16.4	82.0	4990	10	US-09-845-416-34	Sequence 34, Appl
40	16.4	82.0	5060	10	US-09-845-416-36	Sequence 36, Appl
41	16.4	82.0	5149	10	US-09-845-416-27	Sequence 27, Appl
42	16.4	82.0	5339	17	US-10-149-736-40	Sequence 40, Appl
43	16.4	82.0	5339	19	US-10-964-536-40	Sequence 40, Appl
44	16.4	82.0	5417	17	US-10-149-736-39	Sequence 39, Appl
45	16.4	82.0	5417	19	US-10-964-536-39	Sequence 39, Appl

ALIGNMENTS

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                      GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:       April  3, 2005, 22:11:20 ; Search time 598.018 Seconds
                                          (without alignments)
                                          1273.014 Million cell updates/sec

Title:           US-10-088-666-74
Perfect score:   20
Sequence:        1 gagggaagaagttcctat 20

Scoring table:   IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched:        3239544 seqs, 1903213470 residues

Total number of hits satisfying chosen parameters:        68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       EST:*
                 1: gb_est1:*
                 2: gb_est2:*
                 3: gb_htc:*
                 4: gb_est3:*
                 5: gb_est4:*
                 6: gb_est5:*
                 7: gb_est6:*
                 8: gb_gss1:*
                 9: gb_gss2:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

```
                    %
Result          Query
No.    Score  Match Length DB  ID           Description
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c   1    19   95.0   613   4   BI508715     BI508715 BB170011A
    2    18.4 92.0   419   6   CB764501     CB764501 AMGNNUC:S
    3    18.4 92.0   445   6   CB744432     CB744432 AMGNNUC:N
    4    18.4 92.0   467   4   CB714203     CB714203 AMGNNUC:N
c   5    18.4 92.0   536   8   BH047608     BH047608 RPCI-24-3
    6    18.4 92.0   650   4   BI113486     BI113486 602899395
    7    18.4 92.0   662   5   BQ829603     BQ829603 LL6in2145
c   8    18.4 92.0   665   2   BY742218     BY742218 BY742218
c   9    18.4 92.0   696   2   BE113195     BE113195 UI-R-BJ1-
   10    18.4 92.0   748   7   BG921699     BG921699 602825520
   11    18.4 92.0   796   2   CO397391     CO397391 AGENCOURT
   12    18.4 92.0   881   2   BF123606     BF123606 601760528
c  13    18.4 92.0  1015   3   AK020873     AK020873 Mus muscu
c  14    17.4 87.0   205   4   BF998912     BF998912 MR3-GN015
c  15    17.4 87.0   348   4   BG955594     BG955594 CM4-CT065
c  16    17.4 87.0   374   9   CG639825     CG639825 OST371714
   17    17.4 87.0   425   1   AA317772     AA317772 EST19755
   18    17.4 87.0   429   5   BY455173     BY455173 BY455173
   19    17.4 87.0   454   4   BQ832471     BQ832471 LL6in2111
   20    17.4 87.0   468   1   AL046182     AL046182 DKFZp434C
   21    17.4 87.0   590   4   BM704665     BM704665 UI-E-CI1-
   22    17.4 87.0   595   6   CB177816     CB177816 is21c01.x
   23    17.4 87.0   658   7   CN305165     CN305165 170004250
   24    17.4 87.0   671   5   BX918106     BX918106 BX918106
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                                                                 ALIGNMENTS
c  25    17.4  87.0   736   9   AG165391     AG165391   Pan trogl
   26    17.4  87.0   740   6   CB517692     CB517692   ssalrgb50
   27    17.4  87.0   753   9   CL283567     CL283567   ZMMBBb062
   28    17.4  87.0   843   9   CL865206     CL865206   t2g08be.f
   29    17.4  87.0   958   8   BF344853     BF344853   602014145
   30    17.4  87.0  1026   2   BZ248710     BZ248710   CH230-457
c  31    17    85.0   268   2   BB434970     BB434970   BB434970
   32    17    85.0   296   4   BI296803     BI296803   UI-R-DK0-
c  33    17    85.0   584   1   AU016700     AU016700   AU016700
c  34    17    85.0  1025   9   CL452767     CL452767   ZMMBBb047
   35    16.8  84.0   203   4   BM440965     BM440965   BBed02_SQ
   36    16.8  84.0   240   1   AJ482932     AJ482932   AJ482932
   37    16.8  84.0   240   1   AJ482934     AJ482934   AJ482934
c  38    16.8  84.0   262   8   AQ471789     AQ471789   CITBI-E1-
   39    16.8  84.0   273   5   BX558902     BX558902   BX558902
   40    16.8  84.0   282   5   BU970698     BU970698   HB15G16r
   41    16.8  84.0   293   6   CB078133     CB078133   hj63g02.g
   42    16.8  84.0   300   1   AJ482936     AJ482936   AJ482936
   43    16.8  84.0   300   1   AJ482937     AJ482937   AJ482937
   44    16.8  84.0   334   4   BM497325     BM497325   901179 Av
   45    16.8  84.0   360   1   AJ460905     AJ460905   AJ460905
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OM nucleic - .nucleic search, using sw model

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Run on: April 4, 2005, 14:37:50 ; Search time 0.001 Seconds
                                            (without alignments)
                                            240.300 Million cell updates/sec

Title: us-10-088-666-1
Perfect score: 267
Sequence: 1 tatatggaagtaagacccct.........agtagttggggatcgcccc 267

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 0.5

Searched: 25 seqs, 450 residues

Total number of hits satisfying chosen parameters: 50

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 25 summaries

Database :   lissdb:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	No.	ID	Description
1	20	7.5	20	1		US-08-944-974A-1	Sequence 1, Appli
2	17.4	6.5	20	1		US-09-198-452A-3383	Sequence 3383, Ap
3	15.8	5.9	21	1		US-09-422-978-9420	Sequence 9420, Ap
4	15	5.6	15	1		US-08-461-210-30	Sequence 30, Appl
5	14.2	5.3	20	1		US-09-073-567-15	Sequence 15, Appl
6	14.2	5.3	20	1		US-09-073-567-37	Sequence 37, Appl
7	14.2	5.3	20	1		US-09-198-452A-4575	Sequence 4575, Ap
8	13.4	5.0	15	1		US-08-461-210-29	Sequence 29, Appl
9	13.4	5.0	15	1		US-08-461-210-31	Sequence 31, Appl
10	13.2	4.9	18	1		US-08-450-905B-135	Sequence 135, App
11	13.2	4.9	18	1		US-09-213-768-33	Sequence 33, Appl
12	13.2	4.9	18	1		US-09-161-244-53	Sequence 53, Appl
13	13.2	4.9	18	1		US-07-982-759F-135	Sequence 135, App
14	13.2	4.9	18	1		US-08-584-040-6219	Sequence 6219, Ap
15	13.2	4.9	18	1		US-09-371-772B-2981	Sequence 2981, Ap
16	13.2	4.9	18	1		US-09-544-398B-584	Sequence 584, App
17	13.2	4.9	18	1		US-09-543-771B-584	Sequence 584, App
18	13.2	4.9	18	1		US-09-685-664B-2981	Sequence 2981, Ap
19	13	4.9	16	1		US-09-479-005A-399	Sequence 399, App
20	13	4.9	16	1		US-09-479-005A-400	Sequence 400, App
21	12.8	4.8	18	1		US-08-373-124A-15	Sequence 15, Appl
22	12.8	4.8	18	1		US-08-808-303-13	Sequence 13, Appl
23	12.8	4.8	18	1		US-08-435-628-15	Sequence 15, Appl
24	12.8	4.8	18	1		US-09-344-579-10	Sequence 10, Appl
25	12.8	4.8	18	1		US-08-996-533-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1

OM nucleic - nucleic search, using sw model

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Run on: April 4, 2005, 14:39:10 ; Search time 0.001 Seconds
(without alignments)
85.440 Million cell updates/sec

Title: us-10-088-666-1
Perfect score: 267
Sequence: 1 tatatggaagtaagaccct.........agtagttggggatcgcccc 267

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 7 seqs, 160 residues

Total number of hits satisfying chosen parameters: 14

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 7 summaries

Database : 1pubdb:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being princed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	19.2	7.2	25	1	US-10-719-900-325614	Sequence 325614,
2	17.6	6.6	25	1	US-10-719-900-325615	Sequence 325615,
3	17.6	6.6	25	1	US-10-719-900-781674	Sequence 781674,
4	17.4	6.5	20	1	US-10-289-762-3383	Sequence 3383, Ap
c 5	16.2	6.1	22	1	US-10-315-317-24	Sequence 24, Appl
c 6	16.2	6.1	22	1	US-10-315-217-24	Sequence 24, Appl
c 7	15.8	5.9	21	1	US-10-349-143-9420	Sequence 9420, Ap

ALIGNMENTS

```
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OM nucleic - nucleic search, using sw model

Run on:     April  4, 2005, 14:42:29 ; Search time 0.001 Seconds
                                       (without alignments)
                         831.438 Million cell updates/sec

Title:      us-10-088-666-1
Perfect score: 267
Sequence:   1 tatatggaagtaagaccct.........agtagtggggatcgcccc 267

Scoring table: IDENTITY_NUC
             Gapop 10.0 , Gapext 0.5

Searched:   59 seqs, 1557 residues

Total number of hits satisfying chosen parameters:  118

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 59 summaries

Database :  lrngdb:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	267	100.0	267	1	AAF61566	Lactobacillus brev
	2	26.6	10.0	33	1	AAH49988	Bacterial 23S/5S R
	3	25.8	9.7	30	1	AAH50148	Bacterial 23S/5S R
	4	25.8	9.7	30	1	AAH50137	Bacterial 23S/5S R
	5	25.8	9.7	31	1	AAH50158	Bacterial 23S/5S R
	6	25.6	9.6	32	1	AAF61672	Megasphaera sp 23S
	7	25.4	9.5	27	1	AAH50194	Bacterial 23S/5S R
c	8	25	9.4	25	1	AAN80648	Sequence of probe
c	9	25	9.4	25	1	AAN80647	Sequence of probe
	10	25	9.4	25	1	AAF61638	Lactobacillus brev
	11	25	9.4	25	1	AAF61667	Lactobacillus sp 2
	12	23.4	8.8	26	1	AAF61668	Lactobacillus sp 2
c	13	23	8.6	23	1	AAF61618	Unidentified 23S r
	14	23	8.6	32	1	AAF61670	Selenomonas sp 23S
	15	22.8	8.5	31	1	AAH50147	Bacterial 23S/5S R
c	16	21.4	8.0	23	1	AAF61619	Unidentified 23S r
c	17	21.4	8.0	23	1	AAF61616	Unidentified 23S r
c	18	21.4	8.0	23	1	AAF61614	Unidentified 23S r
	19	21	7.9	21	1	AAF61586	Lactobacillus brev
	20	21	7.9	21	1	AAF61664	Lactobacillus sp 2
	21	21	7.9	23	1	AAF61613	Unidentified 23S r
c	22	20.4	7.6	22	1	ABA90523	Lactococcus lactis
	23	20	7.5	20	1	AAQ37096	Lactic acid bacter
	24	20	7.5	20	1	AAQ67115	PCR primer for det
	25	20	7.5	20	1	AAA91894	PCR oligonucleotid
	26	20	7.5	20	1	AAF61663	Lactobacillus sp 2
	27	20	7.5	20	1	AAF61639	Lactobacillus brev
c	28	19.8	7.4	23	1	AAF61615	Unidentified 23S r
c	29	19.8	7.4	23	1	AAF61617	Unidentified 23S r
c	30	19.4	7.3	21	1	AAF61666	Lactobacillus sp 2
	31	19	7.1	27	1	AAH50193	Bacterial 23S/5S R
c	32	18.8	7.0	22	1	ADC21238	Rhodococcus sp est
c	33	18.8	7.0	22	1	ADL22828	X vesicatoria este
c	34	18	6.7	18	1	AAF61628	Unidentified 23S r
	35	17.8	6.7	21	1	AAF61665	Lactobacillus sp 2
	36	17.4	6.5	20	1	AAX94057	PCR primer used to
	37	16.8	6.3	20	1	ADO85452	TaqMan PCR primer
c	38	16.4	6.1	18	1	AAF61626	Unidentified 23S r
c	39	16.4	6.1	18	1	AAF61636	Unidentified 23S r
c	40	16.4	6.1	18	1	AAF61627	Unidentified 23S r
c	41	16.4	6.1	18	1	AAF61632	Unidentified 23S r
c	42	16.2	6.1	22	1	AAH01916	blaTEM resistance
c	43	16.2	6.1	22	1	ADO42863	Primer of the inve
c	44	15.8	5.9	21	1	AAZ75064	Human biallelic ma
	45	15.6	5.8	22	1	AAX27795	Linker for constru
c	46	15.2	5.7	18	1	AAF61625	Unidentified 23S r
	47	15.2	5.7	20	1	ABS52237	Plant vector PCR p
	48	15.2	5.7	21	1	AAZ26236	Human polymorphic
c	49	15	5.6	21	1	ABK97321	#810 5Srev PCR pri
	50	15	5.6	20	1	ABL44318	Human chromosome 1
c	51	14.8	5.5	18	1	AAF61635	Unidentified 23S r
c	52	14.8	5.5	18	1	AAF61631	Unidentified 23S r
c	53	14.8	5.5	18	1	AAF61630	Unidentified 23S r
c	54	14.8	5.5	18	1	AAF61629	Unidentified 23S r
c	55	14.8	5.5	18	1	AAF61634	Unidentified 23S r
	56	14.8	5.5	19	1	AAT92954	Antisense oligonuc
c	57	14.8	5.5	20	1	ADK75919	Chimeric phosphoro
c	58	14.8	5.5	20	1	ADK73951	Chimeric phosphoro
c	59	14.8	5.5	20	1	ADK75223	Chimeric phosphoro

ALIGNMENTS

```
RESULT 1
AAF61566
ID   AAF61566 standard; DNA; 267 BP.
XX
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OM nucleic - nucleic search, using sw model

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Run on:    April 4, 2005, 14:44:14 ; Search time 0.001 Seconds
                                     (without alignments)
                          24.402 Million cell updates/sec

Title:      us-10-088-666-21
Perfect score: 21
Sequence:   1 ccaagtcaacacgtagtgt 21

Scoring table: IDENTITY.NUC
           Gapop 10.0 , Gapext 0.5

Searched:   54 seqs, 581 residues

Total number of hits satisfying chosen parameters:  108

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 60 summaries

Database :   21issdb:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

C	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	13.2	62.9	18	1	US-08-450-905B-135	Sequence 135, App
	2	13.2	62.9	18	1	US-07-982-759F-135	Sequence 135, App
	3	11.8	56.2	15	1	US-08-389-564B-28	Sequence 28, Appl
c	4	11.8	56.2	15	1	US-08-466-047B-28	Sequence 28, Appl
c	5	11.2	53.3	16	1	US-08-303-004-5	Sequence 5, Appli
c	6	9.4	44.8	11	1	US-09-798-542-15	Sequence 15, Appl
c	7	8.8	41.9	15	1	US-08-389-564B-28	Sequence 28, Appl
	8	8.8	41.9	15	1	US-08-466-047B-28	Sequence 28, Appl
c	9	8.4	40.0	10	1	US-08-222-177A-407	Sequence 407, App
	10	8.4	40.0	10	1	US-08-206-176-11	Sequence 11, Appl
c	11	8.4	40.0	10	1	US-08-206-176-11	Sequence 11, Appl
	12	8.4	40.0	10	1	US-08-756-506-10	Sequence 10, Appl
	13	8.4	40.0	10	1	US-08-756-506-10	Sequence 10, Appl
	14	8.4	40.0	10	1	US-09-042-071-28	Sequence 28, Appl
c	15	8.4	40.0	10	1	US-09-042-071-28	Sequence 28, Appl
	16	8.4	40.0	11	1	US-09-249-155A-37	Sequence 37, Appl
	17	8.4	40.0	11	1	US-09-249-155A-266	Sequence 266, App
	18	8.4	40.0	12	1	US-09-427-834A-18	Sequence 18, Appl
c	19	8.0	38.1	10	1	US-09-632-538C-7	Sequence 7, Appli
c	20	8.0	38.1	10	1	US-09-627-536-7	Sequence 7, Appli
c	21	8.0	38.1	10	1	US-09-641-540-7	Sequence 7, Appli
	22	8.0	38.1	11	1	US-08-327-516-8	Sequence 8, Appli
	23	8.0	38.1	11	1	US-09-281-766-8	Sequence 8, Appli
	24	8.0	38.1	11	1	US-09-612-858-8	Sequence 8, Appli
	25	8.0	38.1	11	1	US-09-957-995A-8	Sequence 8, Appli
	26	7.8	37.1	11	1	US-09-798-542-15	Sequence 15, Appl
	27	7.4	35.2	10	1	US-09-263-790-35	Sequence 35, Appl
	28	7.4	35.2	10	1	US-09-721-777-17	Sequence 17, Appl
c	29	7.4	35.2	10	1	US-08-171-718-49	Sequence 49, Appl
c	30	7.4	35.2	10	1	US-08-478-087-49	Sequence 49, Appl
c	31	7.4	35.2	10	1	US-08-522-384-7	Sequence 7, Appli
c	32	7.4	35.2	10	1	US-08-522-384-19	Sequence 19, Appl
c	33	7.4	35.2	10	1	US-08-522-384-82	Sequence 82, Appl
c	34	7.4	35.2	10	1	US-08-927-165A-33	Sequence 33, Appl
c	35	7.4	35.2	10	1	US-09-425-798-14	Sequence 14, Appl
	36	7.4	35.2	10	1	US-09-336-946B-18	Sequence 18, App
	37	7.4	35.2	10	1	US-09-508-753B-145	Sequence 145, App
c	38	7.4	35.2	10	1	US-09-508-753B-221	Sequence 221, App
	39	7.4	35.2	10	1	US-09-508-753B-249	Sequence 249, App
c	40	7.4	35.2	10	1	US-08-894-454-154	Sequence 154, App
	41	7	33.3	10	1	US-08-586-875-2	Sequence 2, Appli
	42	7	33.3	10	1	US-08-631-751A-13	Sequence 13, Appl
	43	7	33.3	10	1	US-08-828-010-4	Sequence 4, Appli
c	44	7	33.3	10	1	US-08-522-384-8	Sequence 8, Appli
c	45	7	33.3	10	1	US-08-522-384-23	Sequence 23, Appl
c	46	7	33.3	10	1	US-08-988-384-2	Sequence 2, Appli
	47	7	33.3	10	1	US-08-991-789A-88	Sequence 88, Appl
	48	7	33.3	10	1	US-09-062-451-88	Sequence 88, Appl
	49	7	33.3	10	1	US-09-598-326-88	Sequence 88, Appl
	50	7	33.3	10	1	US-09-154-750A-25	Sequence 25, Appl
c	51	7	33.3	10	1	US-09-914-259-125	Sequence 125, App
	52	7	33.3	10	1	US-09-508-753B-376	Sequence 376, App
c	53	7	33.3	10	1	US-09-508-753B-436	Sequence 436, App
	54	7	33.3	10	1	US-10-003-830-2	Sequence 2, Appli
c	55	7	33.3	10	1	US-09-289-198-88	Sequence 88, Appl
	56	7	33.3	10	1	US-09-429-755-88	Sequence 88, Appl
c	57	7	33.3	10	1	US-09-822-250A-13	Sequence 13, Appl
	58	7	33.3	10	1	US-10-034-350A-13	Sequence 13, Appl
	59	7	33.3	10	1	US-09-699-295-88	Sequence 88, Appl
c	60	7	33.3	10	1	5244792-18	Patent No. 5244792